SEQUENCE LISTING

<110> University of Utah Research Foundation
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<120> O-Superfamily Conotoxin Peptides

<130> 2714-007

<140> US 09/748,637
<141> 2000-12-26

<150> US 60/243,412
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<150> US60/219,440
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<150> US 60/214,263
<151> 2000-06-26

<150> US 60/173,754
<151> 1999-12-30

<160> 409

<170> PatentIn version 3.0

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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

ttg gca ttc gtc acg gct gat gac tcc gga aat gga atg gag att ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
20 25 30

cgg aag gcg ggt cac gaa atg gag aac ctc gaa gtc tct aat cgg 144
Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
35 40 45

aaa tct tgc cgt aaa gaa ggt caa ctt tgt gat ccg ata ttt caa 192
Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
50 55 60

tgt tgc cgt ggc tgg aat tgc gtt ctt ttc tgc gtc tgaaactacc 241
Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val
65 70 75

261

gtgattnctt ctctccctc

<210> 2
<211> 77
<212> PRT
<213> Conus gloriamaris

<400> 2
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Ile Leu
20 25 30

Pro Pro Lys Ala Gly His Glu Met Glu Asn Leu Glu Val Ser Asn Arg
35 40 45

Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln
50 55 60

Asn Cys Cys Arg Gly Trp Asn Cys Val Leu Phe Cys Val
65 70 75

<210> 3
<211> 29
<212> PRT
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<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp or bromo-Trp

<400> 3
Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
1 5 10 15

Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val
20 25

<210> 4
<211> 29
<212> PRT
<213> Conus gloriamaris

<220>
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<222> (1)..(29)
<223> Xaa at residues 3 and 13 may be pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 15 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 22 may be Trp or bromo-Trp

<400> 4
Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Xaa Gln
1 5 10 15

Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Phe Cys Val
20 25

<210> 5
<211> 29

<212> PRT
<213> Conus gloriamaris

<220>
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<222> (1)..(29)
<223> Xaa at residues 3 and 12 may be pro or hydroxy-Pro; Xaa at residu
e 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may be Trp
or bromo-Trp; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo
-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 5
Val Lys Xaa Cys Arg Lys Xaa Gly Gln Leu Cys Asp Xaa Ile Phe Gln
1 5 10 15

Asn Cys Cys Arg Gly Xaa Asn Cys Val Leu Xaa Cys Val
20 25

<210> 6
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<213> Conus omaria

<220>
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<222> (146)..(235)

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tcgatctgtc catccatcca ttcattcatt cgctgcgaga ctataataaa cattcaagtc 120

tgcattttct ttttgtctg acaga tcg atc agg atg tgc cgt aga gaa gct 172
Ser Ile Arg Met Cys Arg Arg Glu Ala
1 5

caa ctt tgt gat ccg att ttt caa aac tgc tgc cat ggc ttg ttt tgc 220
Gln Leu Cys Asp Pro Ile Phe Gln Asn Cys Cys His Gly Leu Phe Cys
10 15 20 25

gtt ttg gtc tgc gtc taaaactacc gtgatgtctt ctcctcccct ctagtagtag 275
Val Leu Val Cys Val
30

tagggcggcg ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt 335

ctatagtgtc acctaaatta aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa 395

accctggcgt tacccaactt aatcgccttg cagcacatcc cccttttcgcc agctggcgta 455

atagcgaaga ggcccgcacc gatcgccctt cccaacagtt gcgcagcctg aatggcgaat 515

ggaacgcgcc ctgtagcggc gcattat 542

<210> 7
<211> 30
<212> PRT
<213> Conus omaria

<400> 7
Ser Ile Arg Met Cys Arg Arg Glu Ala Gln Leu Cys Asp Pro Ile Phe
1 5 10 15

Gln Asn Cys Cys His Gly Leu Phe Cys Val Leu Val Cys Val
20 25 30

20 25 30

<213> 8
<211> 27
<212> PRT
<213> Conus omaria

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 5 is Glu or gamma-carboxy-Glu; Xaa at residue 11 may be Pro or hydroxy-Pro

<400> 8
Met Cys Arg Arg Xaa Ala Gln Leu Cys Asp Xaa Ile Phe Gln Asn Cys
1 5 10 15

Cys His Gly Leu Phe Cys Val Leu Val Cys Val
20 25

<210> 9
<211> 346
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (25)..(315)

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Met Lys Leu Thr Cys Met Met Ile Val
1 5

gct gtc ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gat gac tcc 99
Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser
10 15 20 25

aga aat gga atg gag aat ctt ttt ccg aag gca ggt cac gaa atg gag 147
Arg Asn Gly Met Glu Asn Leu Phe Pro Lys Ala Gly His Glu Met Glu
30 35 40

aac ctt gaa gac tct aaa cac agg cac cag gag aga ccg gac acc ggc 195
Asn Leu Glu Asp Ser Lys His Arg His Gln Glu Arg Pro Asp Thr Gly
45 50 55

aat aaa gaa gag atg ctg cta cag aga cag gtc aag ccg tgt cgt aaa 243
Asn Lys Glu Glu Met Leu Leu Gln Arg Gln Val Lys Pro Cys Arg Lys
60 65 70

gga cat caa ctt tgt gat ctg att ttt caa aac tgc tgc cgt ggc tgg 291
Gly His Gln Leu Cys Asp Leu Ile Phe Gln Asn Cys Cys Arg Gly Trp
75 80 85

tat tgc gtt gtt ctg tct tgc act tgaaagctac ctgatgtgtt ctactcccat 345
Tyr Cys Val Val Leu Ser Cys Thr
90 95

a 346

<210> 10
<211> 97
<212> PRT
<213> Conus textile

<400> 10
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

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20 25 30

Phe Trp Lys Ala Gly His Glu Met Glu Asn Leu Glu Asp Ser Lys His
35 40 45

Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
50 55 60

Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
65 70 75 80

Ile Ile Gln Asn Cys Cys Arg Gly Trp Tyr Cys Val Val Leu Ser Cys
85 90 95

Thr

<210> 11
<211> 31
<212> PRT
<213> Conus textile

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 8 may be Glu or gamma-carboxy-Glu; Xaa at residue 23 may be Trp or bromo-Trp; Xaa at residue 24

<220>
<221> SITE
<222> (1)..(31)
<223> may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 11
Xaa Val Lys Xaa Cys Arg Lys Xaa His Gln Leu Cys Asp Leu Ile Phe
1 5 10 15

Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Val Val Leu Ser Cys Thr
20 25 30

<210> 12
<211> 265
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (1)..(234)

<400> 12
atg aaa ctg acg tgc ctg atg atc gtt gcc gtg ctg tcc ttg acc ggc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Ser Leu Thr Gly
1 5 10 15

tgg aca ttc gtc acg gct gat gac tct gga aat gga ttg ggg aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu
20 25 30

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ttt ttg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg      144
Phe Leu Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35                  40                  45

aac aag agg tgc gtt cca cac gag ggc cct tgt aat tgg ctt aca caa      192
Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln
    50                  55                  60

aat tgc tgc agt ggt tat aat tgc atc att ttt ttc tgc cta              234
Asn Cys Cys Ser Gly Tyr Asn Cys Ile Ile Phe Phe Cys Leu
65                  70                  75

taaaattacc gtgatgtctt ctcttccact c                                   265
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<210> 13
<211> 78
<212> PRT
<213> Conus cmaria

<400> 13
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Ser Leu Thr Gly
1   5   10   15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Gly Asn Leu
            20   25   30

Phe Leu Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35   40   45

Asn Lys Arg Cys Val Pro His Glu Gly Pro Cys Asn Trp Leu Thr Gln
    50   55   60

Asn Cys Cys Ser Gly Tyr Asn Cys Ile Ile Phe Phe Cys Leu
65   70   75

<210> 14
<211> 27
<212> PRT
<213> Conus cmaria

<220>
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<222> (1)..(27)
<223> Xaa at residues 3 and 7 may be Pro or hydroxy-Pro; Xaa at residue 10 may be Trp or Glu or gamma-carboxy-Glu; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 14
Cys Val Xaa His Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys
1   5   10   15

Leu Gly Xaa Asn Cys Ile Ile Phe Phe Cys Leu
            20   25

<210> 15
<211> 341
<212> DNA
<213> Conus dalli

<220>
<221> CDS
<222> (1)..(291)
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1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
20 25 30

ttt ccg aag gca cgt cac gaa atg gag aac ctc gaa gac tct aaa cac 144
Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
35 40 45

agg cac cag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192
Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
50 55 60

cag aga cag gtc aag ccg tgt cgt aaa gaa cat caa ctt tgt gat ctg 240
Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
65 70 75 80

att ttt caa aac tgc tgc cgt ggc tgg tat tgc ttg ctt cgt cct tgc 288
Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Leu Leu Arg Pro Cys
85 90 95

att tttaaaactacc gtgatgtctt ctctccatc 321
Ile

<210> 16
<211> 97
<212> PRT
<213> Conus dalli

<400> 16
Met Lys Leu Thr Cys Leu Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
35 40 45

Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
50 55 60

Gln Arg Gln Val Lys Pro Cys Arg Lys Glu His Gln Leu Cys Asp Leu
65 70 75 80

Ile Phe Gln Asn Cys Cys Arg Gly Trp Tyr Cys Leu Leu Arg Pro Cys
85 90 95

Ile

<210> 17
<211> 31
<212> PRT
<213> Conus dalli

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 4 and 29
may be Pro or hydroxy-Pro; Xaa at residue 8 may be Glu or gamma-

carboxy-Glu ; Xaa at residue 23 may be Trp or bromo-Trp;

<220>
<221> SITE
<222> (1)..(21)
<223> Xaa at residue 24 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-T
yr, O-sulpho-Tyr or O-phospho-Tyr

<400> 17
Xaa Val Lys Xaa Cys Arg Lys Xaa His Gln Leu Cys Asp Leu Ile Phe
1 5 10 15

Gln Asn Cys Cys Arg Gly Xaa Xaa Cys Leu Leu Arg Xaa Cys Ile
20 25 30

<210> 18
<211> 321
<212> DNA
<213> Conus dalli

<220>
<221> CDS
<222> (1)..(291)

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Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc gga aat gga atg gag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
20 25 30

ttt ccg aag gca cgt cac gaa atg gag aac ctc gaa gac tct aaa cac 144
Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
35 40 45

agg cac cag gag aga ccg gac acg ggc gac aaa gaa gag atg ctg cta 192
Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
50 55 60

cag aga cgg gtc aag ccg tgc agt gaa gaa ggt caa ctt tgt gat cca 240
Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro
65 70 75 80

ctt tct caa aac tgc tgc cgt ggc tgg cat tgc gtt ctt gtc tct tgc 288
Leu Ser Gln Asn Cys Cys Arg Gly Trp His Cys Val Leu Val Ser Cys
85 90 95

321
ctc tgaaactacc gtgatgtctt ctctcccatc
Met
1

<210> 19
<211> 97
<212> PRT
<213> Conus dalli

<400> 19
Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Met Glu Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Glu Asn Leu Glu Asp Ser Lys His
35 40 45

Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
50 55 60

Gln Arg Arg Val Lys Pro Cys Ser Glu Glu Gly Gln Leu Cys Asp Pro
65 70 75 80

Leu Ser Gln Asn Cys Cys Arg Gly Trp His Cys Val Leu Val Ser Cys
85 90 95

Val

<210> 20
<211> 30
<212> PRT
<213> Conus dalli

<220>
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<222> (1)..(30)
<223> Xaa at residues 3 and 15 may be Pro or hydroxy-Pro; Xaa at residues 6 and 7 may be Glu or gamma-carboxy-Glu ; Xaa at residue 22 may be Trp or bromo-Trp

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1 5 10 15

Asn Cys Cys Arg Gly Xaa His Cys Val Leu Val Ser Cys Val
20 25 30

<210> 21
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<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (14)..(347)

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1 5 10

ttc ttg acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga 97
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
15 20 25

ttg ggg aat ctt ttt tcg aat gca cat cac gaa atg aag aac ccc gaa 145
Leu Gly Asn Leu Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu
30 35 40

ccc tct aaa ttg aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt 193
Ala Ser Lys Leu Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys
45 50 55 60

aat ttg tta gac caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc 241
Asn Leu Leu Asp Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val
65 70 75

tgc aca taaaactgcc gtgatgtctt ctcttcccct ctgtgctacc tggcttgatc 297

Cys Thr

ttgatggc gcgtgtcgtt cactggttat gaacccccc ccccccccc ccccccccct 357

tcggctctc tggaggcctc gggggttcaa catccaaata aagtgacag 406

<210> 22
<211> 78
<212> PRT
<213> Conus textile

<400> 22
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

<210> 23
<211> 27
<212> PRT
<213> Conus textile

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 23
Xaa Cys Lys Gln Asp Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

<210> 24
<211> 27
<212> PRT
<213> Conus textile

<220>
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<222> (1)..(26)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu;Xaa at residue 9 is Nle; Xaa at residue 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 24
Xaa Cys Lys Gln Asp Gly Xaa Xaa Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

<211> 85
<212> DNA
<213> Conus magus

<220>
<221> CDS
<222> (1)..(234)

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Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc tgc aca 234
Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

taaaactgca gtgatgtctt ctcctccact g 265

<210> 26
<211> 78
<212> PRT
<213> Conus magus

<400> 26
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

<211> 27
<212> PRT
<213> Conus magus

<220>
<221> SITE
<222> (1)..(27)

<...> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<...> 17
Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

<210> 28
<211> 27
<212> PRT
<213> Conus textile

<220>
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<222> (1)..(27)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 18
Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Phe Val Cys Thr
20 25

<210> 29
<211> 265
<212> DNA
<213> Conus distans

<220>
<221> CDS
<222> (1)..(234)

<400> 19
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Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

ttc tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

caa aac tgc tgc gac ggc tat tgc ata gta ctt gtc tgc aca 234
Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

tgaaactgcc gtgatgtctt ctcctccact c 265

<210> 30
<211> 78

<110> PPT
<111> Conus distans

<400> 30
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

<210> 31
<211> 27
<212> PRT
<213> Conus distans

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 31
Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

<210> 32
<211> 265
<212> DNA
<213> Conus ammiralis

<220>
<221> CDS
<222> (1)..(234)

<400> 32
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

ttc tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac 192
Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

234

caa aac tgc tgc gag ggc tat tgc ata gta ctt gtc tgc aca
Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

265

taaaatgcc gtgatgtctt ctcctccact c

<211> 33
<212> PRT
<213> Conus ammiralis

<400> 33
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Ile Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
50 55 60

Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
65 70 75

<210> 34
<211> 27
<212> PRT
<213> Conus ammiralis

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 7 and 1
9 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr,
125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
-Tyr

<400> 34
Xaa Cys Lys Gln Ser Gly Xaa Met Cys Asn Leu Leu Asp Gln Asn Cys
1 5 10 15

Cys Xaa Gly Xaa Cys Ile Val Leu Val Cys Thr
20 25

<210> 35
<211> 156
<212> DNA
<213> Conus dalli

<220>
<221> CDS
<222> (1)..(135)

<400> 35
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

```
ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct aag ttg aat      144
Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
        35                  40                  45

gaa agg tgc ctt ggt ggt ggt gaa gtt tgt gat atc ttt ttt cca caa      192
Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln
    50                  55                  60

tgc tgt ggc tat tgc att ctt ctt ttc tgc aca taaaactacc gtgatgtctt    245
Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr
65                  70                  75

gtttttcct c                                                         256

<210>  36
<211>  75
<212>  PRT
<213>  Conus dalli

<400>  36
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                   10                  15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
            20                  25                  30

Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
        35                  40                  45

Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln
    50                  55                  60

Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr
65                  70                  75

<210>  37
<211>  25
<212>  PRT
<213>  Conus dalli

<220>
<221>  SITE
<222>  (1)..(25)
<223>  Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
       18 may be Pro or hydroxy-Pro;Xaa at residue 18 may be Tyr, 125-I-
       Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400>  37
Cys Leu Gly Gly Gly Xaa Val Cys Asp Ile Phe Phe Xaa Gln Cys Cys
1               5                   10                  15

Gly Xaa Cys Ile Leu Leu Phe Cys Thr
            20                  25

<210>  38
<211>  441
<212>  DNA
<213>  Conus gloriamaris

<220>
<221>  CDS
<222>  (70)..(300)

<400>  38
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gcttgcacgg tgaatttggc ttcacagttt tccactgtcg tctttggcat catctgaaac 60

atcgccaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg 111
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 159
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly
15 20 25 30

aat att ttt tcg aat gca cat cac gaa atg aag aat ccc gaa gcc tct 207
Asn Ile Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ttg aac aag agg tgc cgt cta ggg gct gaa agt tgt gat gta att 255
Lys Leu Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile
50 55 60

tca caa aac tgc tgc caa ggc acg tgc gtt ttt ttc tgc tta cca 300
Ser Gln Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro
65 70 75

tgatgtcttc tattctcctc tgtgctacct ggcttgatct ttcattagcg cgtgcctttc 360

acttgtttatg aaccccctga tccgactctc tggcagcctc gggggttcaa catccaaata 420

aaaaaaaaaa acaatgacaa a 441

<210> 39
<211> 77
<212> PRT
<213> Conus gloriamaris

<400> 39
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Ile
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Arg Leu Gly Ala Glu Ser Cys Asp Val Ile Ser Gln
50 55 60

Asn Cys Cys Gln Gly Thr Cys Val Phe Phe Cys Leu Pro
65 70 75

<210> 40
<211> 26
<212> PRT
<213> Conus gloriamaris

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 26 may be Pro or hydroxy-Pro

<400> 40
Cys Arg Leu Gly Ala Xaa Ser Cys Asp Val Ile Ser Gln Asn Cys Cys
1 5 10 15

Gln Gly Thr Cys Val Phe Phe Cys Leu Xaa
20 25

<220> 41
<211> 446
<212> DNA
<213> Conus gloriamaris

<220>
<221> CDS
<222> (74)..(304)

<400> 41
ggatcctgc acggtgaatt tggcttcaca gttttccact gtcgtctttc gcatcatcca 60

aaacatcacc aag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg 109
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu
1 5 10

ttc ttg acc gcc tgg aca ttc gcc acg gct gat gac ccc aga aat gga 157
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
15 20 25

ttg gag aaa ctt ttt tcg aat aca cat cac gaa atg aag aac ccc gaa 205
Leu Glu Lys Leu Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu
30 35 40

gct tct aaa ttg aac aag agg tgc aaa caa gct gat gaa tct tgt aat 253
Ala Ser Lys Leu Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn
45 50 55 60

gta ttt tca ctt gac tgc tgc acc ggc tta tgc ttg gga ttc tgc gta 301
Val Phe Ser Leu Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val
65 70 75

tcg tgatgtcttc tactcccctc tgtgctacct ggcttgatct ttgattggcg 354
Ser

tgtgccttta atggttatg aaccccccctg atccgattct ttggcggcct cgggggttca 414

acatccaaat aaagcgacag cacaataaaa aa 446

<210> 42
<211> 77
<212> PRT
<213> Conus gloriamaris

<400> 41
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Lys Leu
20 25 30

Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn Val Phe Ser Leu
50 55 60

Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val Ser
65 70 75

<400> 43
Cys Lys Gln Ala Asp Xaa Ser Cys Asn Val Phe Ser Leu Asp Cys Cys
1 5 10 15
Thr Gly Leu Cys Leu Gly Phe Cys Val Ser
20 25

<210> 44
<211> 242
<212> DNA
<213> Conus gloriamaris

<220>
<221> CDS
<222> (1)..(225)

<400> 44
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc acc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

tgg acg ttc gcc acg gcc atc acc agg aat gga ttg ggg aat ctt ttt 96
Trp Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe
20 25 30

ccg aag aat cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg aac 144
Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn
35 40 45

aag agg tgc gtt cca tac gag ggc cct tgt aat tgg ctt aca caa aac 192
Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn
50 55 60

tgc tgc gat gag cta tgc gta ttt ttc tgc cta taaaactagc ctgatgt 242
Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu
65 70 75

<210> 45
<211> 75
<212> PRT
<213> Conus gloriamaris

<400> 45
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

Trp Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe
20 25 30

Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn
35 40 45

Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn
50 55 60

Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu
65 70 75

<220> 46
<221> 25
<212> PRT
<213> Conus gloriamaris

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 2 and 7 may be Pro or hydroxy-Pro; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 and 18 may be Glu or gamma-carboxy-Glu ; Xaa at residue 10 may be Trp or bromo-Trp

<400> 46
Cys Val Xaa Xaa Xaa Gly Xaa Cys Asn Xaa Leu Thr Gln Asn Cys Cys
1 5 10 15

Asp Xaa Leu Cys Val Phe Phe Cys Leu
20 25

<210> 47
<211> 250
<212> DNA
<213> Conus magus

<220>
<221> CDS
<222> (1)..(231)

<400> 47
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctc ttc ttg acc gtc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val
1 5 10 15

tgg aca ttc gcc acg gct gat gac tcc gga aat gga ttg gag aaa ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
20 25 30

ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgc aaa caa gct gat gaa ccc tgt gat gta ttt tca ctt 192
Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu
50 55 60

gga tgc tgc acc ggc ata tgt ctt gga ttc tgc acg tgg tgatgtcttc 241
Gly Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp
65 70 75

aaaaaaaaaa aaaaaaaaaa 250

<210> 48
<211> 77
<212> PRT
<213> Conus magus

<400> 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Val
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
20 25 30

Phe Cys Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu
50 55 60

Gln Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp
65 70 75

<210> 49
<211> 26
<212> PRT
<213> Conus magus

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 and 14 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 7 may be Pro or hydroxy-Pro; Xaa at residue 26may be Trp o
r bromo-Trp

<400> 49
Cys Lys Gln Ala Asp Xaa Xaa Cys Asp Val Phe Ser Leu Xaa Cys Cys
1 5 10 15

Thr Gly Ile Cys Leu Gly Phe Cys Thr Xaa
20 25

<210> 50
<211> 434
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (71)..(295)

<400> 50
ccatttgcaag gtgaatttgg cttcatagtt ttccactgtc gtctttggca tcatccaaaa 60

gatgaccaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc 109
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe
1 5 10

ttg acc gcc tgg aca ttc gcc acg gct gat gac tcc agc aat gga ttg 157
Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu
15 20 25

gag aac ctt ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct 205
Glu Asn Leu Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser
30 35 40 45

aag ttg aac gag agg tgc ctt gat gct ggt gaa gtt tgt gat att ttt 253
Lys Leu Asn Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe
50 55 60

ttt cca aca tgc tgc ggc tat tgc att ctt ctt ttc tgc gca 295
Phe Pro Thr Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala
65 70 75

taaaactacc gtgatgtctt ctactccact ctgtgctacc tggcttgatc tttgattggc 355

gcgtacgcgtt cactggttat gaaaccccctg atccagctct ctggaggcct cggggttca 415

acgtcgaaat aaaggcgaca 434

<210> 51
<211> 75
<212> PRT
<213> Conus textile

<400> 51
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu
20 25 30

Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
35 40 45

Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe Phe Pro Thr
50 55 60

Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala
65 70 75

<210> 52
<211> 25
<212> PRT
<213> Conus textile

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

<400> 52
Cys Leu Asp Ala Gly Xaa Val Cys Asp Ile Phe Phe Xaa Thr Cys Cys
1 5 10 15

Gly Xaa Cys Ile Leu Leu Phe Cys Ala
20 25

<210> 53
<211> 26
<212> PRT
<213> Conus textile

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at residue 7 may be Pro or hydroxy-Pro

<400> 53
Cys Ile Xaa Gln Phe Asp Xaa Cys Xaa Met Ile Arg His Thr Cys Cys
1 5 10 15

Val Gly Val Cys Phe Leu Met Ala Cys Ile
20 25

<210> 54
<211> 26

<220>
<221> PPT
<222> Conus textile

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3, 7 and 13 may be Pro or hydroxy-Pro; Xaa at residue 14 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 54
Cys Ala Xaa Phe Leu His Xaa Cys Thr Phe Phe Phe Xaa Asn Cys Cys
1 5 10 15

Asn Ser Xaa Cys Val Gln Phe Ile Cys Leu
20 25

<210> 55
<211> 260
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (1)..(240)

<400> 55
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ttt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
20 25 30

ttt tcg aag aca caa cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgc cta gca gaa cat gaa act tgt aat ata ttt aca caa 192
Asn Lys Arg Cys Leu Ala Glu His Glu Thr Cys Asn Ile Phe Thr Gln
50 55 60

aac tgc tgc gaa ggc gtg tgc att ttt atc tgc gta caa gct cca gag 240
Asn Cys Cys Glu Gly Val Cys Ile Phe Ile Cys Val Gln Ala Pro Glu
65 70 75 80

ctgatgtattc tcctccccctc 260

<210> 56
<211> 80
<212> PRT
<213> Conus omaria

<400> 56
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
20 25 30

Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Ala Glu His Glu Thr Cys Asn Ile Phe Thr Gln
50 55 60

Asn Cys Cys Glu Gly Val Cys Ile Phe Ile Cys Val Gln Ala Pro Glu
65 70 75 80

<210> 57
<211> 29
<212> PRT
<213> Conus omaria

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 4, 6, 17 and 29 may be Glu or gamma-carboxy-Glu;
Xaa at residue 28 may be Pro or hydroxy-Pro

<400> 57
Cys Leu Ala Xaa His Xaa Thr Cys Asn Ile Phe Thr Gln Asn Cys Cys
1 5 10 15

Xaa Gly Val Cys Ile Phe Ile Cys Val Gln Ala Xaa Xaa
20 25

<210> 58
<211> 261
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (1)..(231)

<400> 58
atg aaa ctg act gtc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gaa gac ccc aga cat gga ttg gag aat ctt 96
Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu
20 25 30

ttt tcg aag gca cat cac gaa atg aag aac cct gaa gac tct aaa ttg 144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
35 40 45

gac aag agg tgc att cca cat ttt gac cct tgt gac ccg ata cgc cac 192
Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His
50 55 60

acc tgc tgc ttt ggc ctg tgc cta cta ata gcc tgc atc taaaactgcc 241
Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
65 70 75

atgatatctt ctctcccatc 261

<210> 59
<211> 77
<212> PRT
<213> Conus omaria

<400> 59
Met Lys Leu Thr Val Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
35 40 45

Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His
50 55 60

Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
65 70 75

<210> 60
<211> 26
<212> PRT
<213> Conus omaria

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.

<400> 60
Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys
1 5 10 15

Thr Gly Leu Cys Leu Leu Ile Ala Cys Ile
20 25

<210> 61
<211> 259
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (1)..(228)

<400> 61
atg aaa ctg acg tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gaa gac ccc aga gat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu
20 25 30

tct tca aat gca cat aac gaa atg aag aac ccc gaa gcc tct aca ttg 144
Leu Ser Asn Ala His Asn Glu Met Lys Asn Pro Glu Ala Ser Thr Leu
35 40 45

aac gaa agg tgc ctt ggg ttt ggt gaa gct tgt ctt ata ctt tat tca 192
Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Ile Leu Tyr Ser
50 55 60

ttc tgc tgc ggc tat tgc gtt ggt gct atc tgc cta taaaactacc 238
Phe Cys Cys Gly Tyr Cys Val Gly Ala Ile Cys Leu
65 70 75

ggaagtatt ctcctccact c 259

<210> 62
<211> 76
<212> PRT

<...> Conus omaria

<...> 62
Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu
20 25 30

Leu Ser Asn Ala His Asn Glu Met Lys Asn Pro Glu Ala Ser Thr Leu
35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Ile Leu Tyr Ser
50 55 60

Asp Cys Cys Gly Tyr Cys Val Gly Ala Ile Cys Leu
65 70 75

<...> 63
<...> 25
<...> PRT
<...> Conus omaria

<...>
<...> SITE
<...> (1)..(25)
<...> Xaa at residue may be Glu or gamma-carboxy-Glu; Xaa at residues
11 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s
ulpho-Tyr or O-phospho-Tyr

<...> 63
Cys Leu Gly Phe Gly Xaa Ala Cys Leu Ile Leu Xaa Ser Asp Cys Cys
1 5 10 15

Gly Xaa Cys Val Gly Ala Ile Cys Leu
20 25

<...> 64
<...> 162
<...> DNA
<...> Conus aulicus

<...>
<...> CDS
<...> (1)..(240)

<...> 64
atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

ttt tcg aag aca caa cac aaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgc aaa gca gaa aat gaa ctt tgt aat ata ttt ata caa 192
Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln
50 55 60

aac tgt tgc gac ggg acg tgc ctt ctt atc tgc ata caa aat cca cag 240

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln
65 70 75 80

262

tgatgt cttc tctcctaccc tc

<220> 65
<221> 80
<222> PRT
<223> Conus aulicus

<400> 65
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln
50 55 60

Asn Cys Cys Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Pro Gln
65 70 75 80

<220> 66
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 4 and 6may be Glu or gamma-carboxy-Glu; Xaa at residue 28 may be Pro or hydroxy-Pro

<400> 66
Cys Lys Ala Xaa Asn Xaa Leu Cys Asn Ile Phe Ile Gln Asn Cys Cys
1 5 10 15

Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Xaa Gln
20 25

<210> 67
<211> 258
<212> DNA
<213> Conus aulicus

<220>
<221> CDS
<222> (1)..(228)

<400> 67
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gat aat cgt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg
20 25 30

ttt tcg aag gca cgt cac gaa atg aat aac cgc aga gcc tct aaa ttg 144
Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu

35 40 45

aat aag agg tgc ctt gag ttt ggt gaa ctt tgt aat ttt ttt ttc cca 192
Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro
50 55 60

act tgc tgc ggc tat tgc gtt ctt ctt gtc tgc cta taaactaccg 238
Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
65 70 75

tgatgatctg tcttcccctc 258

<210> 65
<211> 76
<212> PRT
<213> Gallus gallicus

<400> 65
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg
20 25 30

Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Glu Phe Gly Glu Leu Cys Asn Phe Phe Phe Pro
50 55 60

Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
65 70 75

<210> 66
<211> 25
<212> PRT
<213> Gallus gallicus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
o-Tyr

<400> 66
Cys Leu Xaa Phe Gly Xaa Leu Cys Asn Phe Phe Phe Xaa Thr Cys Cys
1 5 10 15

Gly Xaa Tyr Val Leu Leu Val Cys Leu
20 25

<210> 70
<211> 363
<212> DNA
<213> Gallus gallus

<220>
<221> CDS
<222> (1)..(231)

<400> 70
atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48

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Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

tgg aca ttt gtc atg gct gat gac tcc gga aat gga ttg gaa aat ctg      96
Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
            20                  25                  30

ttt tcg aag gca cat cac gaa atg aag aac cct gaa gcc tct aaa ttg     144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35                  40                  45

aac aag agg tgc gct caa agc agt gaa tta tgt gat gcg ctg gac tca     192
Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser
    50                  55                  60

gac tgc tgc agt ggt gtt tgc atg gta ttt ttc tgc cta taaaactgcc     241
Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu
65                  70                  75

gtggatgtctt ctctatcccc tc                                         263
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<200> 71
<211> 77
<212> PRT
<213> Conus dalli

<400> 71
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1   5   10   15

Trp Thr Phe Val Met Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
            20   25   30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35   40   45

Asn Lys Arg Cys Ala Gln Ser Ser Glu Leu Cys Asp Ala Leu Asp Ser
    50   55   60

Asp Cys Cys Ser Gly Val Cys Met Val Phe Phe Cys Leu
65   70   75

<210> 72
<211> 26
<212> PRT
<213> Conus dalli

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu.

<400> 72
Cys Ala Gln Ser Ser Xaa Leu Cys Asp Ala Leu Asp Ser Asp Cys Cys
1   5   10   15

Cys Gly Val Cys Met Val Phe Phe Cys Leu
            20   25

<210> 73
<211> 259
<212> DNA
<213> Conus distans

<210>
<211> CDS
<212> (1)..(229)

<400> 73
atg aaa ctg acg tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg acg ttc gtc acg gct gaa gac ccc aga gat gga ttg agg aat ctt 96
Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu
20 25 30

tta tcg aat gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac gag agg tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt tat tca 192
Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
50 55 60

gac tgc tgc agc tat tgc gtt ggt gct gtc tgc cta taaaactacc 238
Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu
65 70 75

atgatgtctt ctactcccat 259

<210> 74
<211> 76
<212> PRT
<213> Conus distans

<400> 74
Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu
20 25 30

Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
50 55 60

Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu
65 70 75

<210> 75
<211> 25
<212> PRT
<213> Conus distans

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residues 12 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulphi-Tyr or O-phospho-Tyr

<400> 75
Cys Leu Gly Phe Gly Xaa Ala Cys Leu Met Leu Xaa Ser Asp Cys Cys
1 5 10 15

Ser Xaa Cys Val Gly Ala Val Cys Leu
20 25

<211> 76
<212> DNA
<213> Conus pennaceus

<220>
<221> CDS
<222> (1)..(231)

<400> 76
Met Lys Leu Thr Cys Leu Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
35 40 45

Asp Lys Arg Cys Val Lys Tyr Leu Asp Pro Cys Asp Met Leu Arg His
50 55 60

Thr Cys Cys Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
65 70 75

<210> 77
<211> 77
<212> PRT
<213> Conus pennaceus

<400> 77
Met Lys Leu Thr Cys Leu Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
35 40 45

Asp Lys Arg Cys Val Lys Tyr Leu Asp Pro Cys Asp Met Leu Arg His
50 55 60

Thr Cys Cys Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
65 70 75

<210> 78
<211> 26
<212> PRT
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(26)

<...> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or
hydroxy-Pro

<4...> 78
Cys Val Lys Xaa Leu Asp Xaa Cys Asp Met Leu Arg His Thr Cys Cys
1 5 10 15

Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
20 25

<...10> 79
<...11> 259
<...12> DNA
<...13> Conus pennaceus

<...0>
<...21> CDS
<...22> (1)..(238)

<...00> 79
atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg acg ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gct tct aaa ttg 144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac gag agg tgc ctt ggg ttt ggt gaa gtt tgc aat ttc ttt ttt cca 192
Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro
50 55 60

aac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta taaaactacc 238
Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

gtaatgtctt ctattccact c 259

<...00> 80
<...11> 76
<...12> PRT
<...13> Conus pennaceus

<...00> 80
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Phe Pro
50 55 60

Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

<210> 81
<211> 25
<212> PRT
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 81
Cys Leu Gly Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Asn Cys Cys
1 5 10 15

Ser Xaa Cys Val Ala Leu Val Cys Leu
20 25

<210> 82
<211> 240
<212> DNA
<213> Conus pennaceus

<220>
<221> CDS
<222> (1)..(240)

<400> 82
atg aaa ctg acg tgc gtg atg ctc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Leu Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gcc acg gct gat gac tcc agc aat gga ctg gag aat ctt 96
Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu
20 25 30

ttc tcg aag gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgc att cca caa ttt gat cct tgt gac atg gta cgt cac 192
Asn Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His
50 55 60

act tgc tgc aaa ggg ttg tgc gta cta ata gcc tgc tct aaa act gcg 240
Thr Cys Cys Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala
65 70 75 80

tgatgtctta atctccgctc 260

<210> 83
<211> 80
<212> PRT
<213> Conus pennaceus

<400> 83
Met Lys Leu Thr Cys Val Met Leu Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu

35 40 45

Asn Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His
50 55 60

Thr Cys Cys Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala
65 70 75 80

<400> 84
<211> 19
<212> PRT
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(24)
<223> Xaa at residues 3 and 7 may be Pro or hydroxy-Pro.

<400> 84
Cys Ile Xaa Gln Phe Asp Xaa Cys Asp Met Val Arg His Thr Cys Cys
1 5 10 15

Lys Gly Leu Cys Val Leu Ile Ala Cys Ser Lys Thr Ala
20 25

<210> 85
<211> 260
<212> DNA
<213> Conus pennaceus

<220>
<221> CDS
<222> (1)..(240)

<400> 85
atg aaa ctg acg tgc ttg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

ttg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ttt 96
Leu Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
20 25 30

atg tcg aag aca caa cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Met Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag agg tgc aaa gca gaa agt gaa gct tgt aat ata att aca caa 192
Asn Lys Arg Cys Lys Ala Glu Ser Glu Ala Cys Asn Ile Ile Thr Gln
50 55 60

aac tgc tgc gac ggc aag tgc ctt ttt ttc tgc ata caa att cca gag 240
Asn Cys Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu
65 70 75 80

tgaaggtgttc tgctcccatc 260

<210> 86
<211> 80
<212> PRT
<213> Conus pennaceus

<400> 86
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
20 25 30

Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Lys Ala Glu Ser Glu Ala Cys Asn Ile Ile Thr Gln
50 55 60

Asn Cys Cys Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Pro Glu
65 70 75 80

<210> 87
<211> 29
<212> PRT
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 4, 6 and 29 may be Glu or gamma-carboxy-Glu; Xaa at residue 28 may be Pro or hydroxy-Pro

<400> 87
Cys Lys Ala Xaa Ser Xaa Ala Cys Asn Ile Ile Thr Gln Asn Cys Cys
1 5 10 15

Asp Gly Lys Cys Leu Phe Phe Cys Ile Gln Ile Xaa Xaa
20 25

<210> 88
<211> 432
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (110)..(199)

<400> 88
ggtcgacatc atcatcatca tcgatccatc tgtccatcca tccattcatt cattcgctgc 60

catactgtca taaatattcg agtctctcct tctgtttgta tctgacaga ttg aac aag 118
Leu Asn Lys
1

agg tgc att gac ggt ggt gaa att tgt gat att ttt ttt cca aac tgc 166
Arg Cys Ile Asp Gly Gly Glu Ile Cys Asp Ile Phe Phe Pro Asn Cys
5 10 15

tgc agt ggg tgg tgc att att ctc gtc tgc gca tgaaactacc gtgatgtctt 219
Cys Ser Gly Trp Cys Ile Ile Leu Val Cys Ala
20 25 30

cgtctctcct ctagtagtag taggcggccg ctctagagga tccaagctta cgtacgcgtg 279

tatgcgacgt catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt 339

acaacgtcgt gactgggaaa accctggcgt tacccaactt aatcgccttg cagcacatcc 399

ccctttcgcc agctggcgta atagcgaaga ggcccgcacc gatcgccctt ccaacagttt 459

gcacagcctg aatggcgaat gggacgcgcc ctgtagcggc gcattaagcg cggcgggtgt 519

ggtgggtacg cgcagcgtga cgggtacact tgccagcgcc ctagcgcccg ctcctttgc 579

ttgttcccct tccttttctcg ccaccgttcg ccgggggttt tcccgtcaag ctc 632

<213> Conus omaria

<400> 89
Leu Asn Lys Arg Cys Ile Asp Gly Gly Glu Ile Cys Asp Ile Phe Phe
1 5 10 15

Phe Asn Cys Cys Ser Gly Trp Cys Ile Ile Leu Val Cys Ala
20 25 30

<213> Conus omaria

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
19 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bro
mo-Trp

<400> 90
Cys Ile Asp Gly Gly Xaa Ile Cys Asp Ile Phe Phe Xaa Asn Cys Cys
1 5 10 15

Cys Gly Xaa Cys Ile Ile Leu Val Cys Ala
20 25

<213> Conus omaria

<220>
<221> CDS
<222> (107)..(196)

<400> 91
ggtcgacatc atcatcatcg atccatctgt ccatccatcc attcattcat tcgctgccag 60

acttgtcaataa atattcgagt ctctccttct gtttgtatct gacaga ttg aac aag 115
Leu Asn Lys
1

agg tgc ctt gac ggt ggt gaa att tgt ggt att ttg ttt cca agc tgc 163
Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro Ser Cys
5 10 15

tgc aat ggg tgg tgc att gtt ctc gtc tgc gca tgaaactacc gtgatgtctt 216
Cys Asn Gly Trp Cys Ile Val Leu Val Cys Ala
20 25 30

gtactttcct ctagtagtag taggcggccg ctctagagga tccaagctta cgtacgcgtg 276

catgcatacgt catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt 336

a[illegible]cgtcgt gactgggaaa accctggcgt tacccaactt aatcgccttg cagcacatcc 396

c[illegible]tc[illegible]gcc agctggcgta atagcgaaga ggcccgcacc gatcgccctt cccaacaagt 456

t[illegible]gcgtgcct gaatggcgaa tgggacgcgc cctgtagcgg cgcattaagc gcggcgggtg 516

t[illegible]gttttac gcgcaccgtg accgctacac ttgccagcgc cctagcgcgc cgctcctttc 576

gctt[illegible]ctc cttcctttct cgcacgttcg gcggctttcc ccgtcaagct ctaaatcgg 636

650

g[illegible]ttcgcct ttta

<210> 92
<211> 26
<212> PRT
<213> Conus omaria

<400> 92
Leu Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe
1 5 10 15

Xaa Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
20 25 30

<210> 93
<211> 26
<212> PRT
<213> Conus omaria

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 19 may be Trp or bromo-Trp

<400> 93
Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys
1 5 10 15

Ser Gly Xaa Cys Ile Val Leu Val Cys Ala
20 25

<210> 94
<211> 618
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (107)..(193)

<400> 94
[illegible]tcgacatc atcatcatcg atccatctgt ccatccatcc atccattcat tcgctgccag 60

[illegible]cgtgaataa atattcgagt ctctctcttct gtttgtatct gacaga ttg aac aag 115
Leu Asn Lys
1

[illegible]gg tgc ctt gag ttt ggt gaa gtt tgt aat ttt ttt ttc cca acc tgc 163
Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe Pro Thr Cys
5 10 15

tgc g[illegible]c tat tgc gtt ctt ctt gtc tgc cta taaaactacc gtgatgtctt 213

Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
20 25

cttctttcct ctagtagtag taggcggccg ctctagagga tccaagctta cgtacgcgtg 273

catgcttccgt catagctctt ctatagtgtc acctaaattc aattcactgg ccgtcgtttt 333

acaacgtcgt gactgggaaa accctggcgt tacccaactt aatcgccttg cagcacatcc 393

ccctttcgcc agctggcgta atagcgaaga ggcccgcacc gatcgccctt cccaacagtt 453

gcgcagcctg aatggcgaat gggacgcgcc ctgtagcggc gcattaagcg cggcgggtgt 513

ggtggttacg cgcagcgtga ccgctacact tgccagcgccc tagcgcccgc tcctttcgct 573

ttcttcccct cctttctcgc cacgttcgcc ggctttcccc gtcaa 618

<210> 95
<211> 29
<212> PRT
<213> Conus marmoreus

<400> 95
Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
1 5 10 15

Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
20 25

<210> 96
<211> 25
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 18 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
o-Tyr

<400> 96
Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys
1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu
20 25

<210> 97
<211> 444
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (150)...(236)

<400> 97
gaaagcctgt acgcctgcag gtaccggtcc ggaattcccg ggtcgacatc atcatcatca 60

tcgatccatc tgtccatcca tccattcatt cattcgctgc cagactgtaa taaatattcg 120

agtttctact tctgtttgta tctgacagg ttg aac aag agg tgc caa gag ttc 173

Leu Asn Lys Arg Cys Gln Glu Phe
1 5

ggt gaa gtt tgt aat ttt ttt ttc cca gac tgc tgc ggc tat tgc gtt 221
Gly Glu Val Cys Asn Phe Phe Phe Pro Asp Cys Cys Gly Tyr Cys Val
10 15 20

ctt tta ctc tgc ata taaaactacc gtgatgtctt ctcttcccat ctagtagtag 276
Leu Leu Leu Cys Ile
25

tagttatagt aggcggcgcgc tctagaggat ccaagcttac gtacgcgtgc atgcgacgtc 336

atagctctcc tatagtgtca cctaaattca attcactggc cgtcgtttta caacgtcgt 396

gactgggaaaa accctggcgt tcccaactta attcgccttg cagcacat 444

<210> 98
<211> 25
<212> PRT
<213> Conus marmoreus

<400> 98
Leu Asn Lys Arg Cys Gln Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
1 5 10 15

Pro Asp Cys Cys Gly Tyr Cys Val Leu Leu Leu Cys Ile
20 25

<210> 99
<211> 25
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 18may be Tyr, residue 13 may be Pro or hydroxy-Pro; Xaa at residue
125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
-Tyr

<400> 99
Cys Gln Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Asp Cys Cys
1 5 10 15

Gly Xaa Cys Val Leu Leu Leu Cys Ile
20 25

<210> 100
<211> 545
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (155)..(242)

<220>
<221> misc_feature
<222> (1)..(545)
<223> n may be any nucleotide

<400> 100

ttttaaggcn ggtacgcctg caggtaccgg tccggaattc ccgggtcgac atcatcatca 60

tcattcatcc atctgtccat ccatccattc attcattcgc taccagactg taataaatat 120

tcaaaaatct ctttctgttt gtatctgaca ga ttg gac aag agg tgc att cca 173
Leu Asp Lys Arg Cys Ile Pro
1 5

cat ttt gac cct tgt gac ccg ata cgc cac acc tgc tgc ttt ggc ctg 221
His Phe Asp Pro Cys Asp Pro Ile Arg His Thr Cys Cys Phe Gly Leu
10 15 20

tgt cta cta ata gcc tgc atc taaaactgcc gtgatgtctt ctcctccccc t 272
Cys Leu Leu Ile Ala Cys Ile
25 30

ctagtagtag taggcgggcg ctctagagga tccaagctta cgtacgcgtg catgcgacgt 332

cataggtctt ctatagtgtc acctaaatic aattcactgg ccgtcgtttt acaacgtcgt 392

gactgggaaa accctggcgt tacccaactt aatcgccttg cagcacatcc ccctttcgcc 452

agctggcgta atagcgaaga ggcccgcacc gatcgccctt cccaacagtt gcgcagcctg 512

aatggcgaat gggacgcgcc ctgtagcggc gct 545

<210> 101
<211> 30
<212> PRT
<213> Conus omaria

<400> 101
Leu Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg
1 5 10 15

His Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
20 25 30

<210> 102
<211> 26
<212> PRT
<213> Conus omaria

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.

<400> 102
Cys Ile Xaa His Phe Asp Xaa Cys Asp Xaa Ile Arg His Thr Cys Cys
1 5 10 15

Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
20 25

<210> 103
<211> 534
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (140)..(226)

<400> 103
ggtacatcctg caggtaccgg tccggaattc ccgggtcgac atcatcatca tcgatccatc 60

tgttcatccca tccattcttt catttgctgc cajactgtaa taaatattcg agtctctctt 120

tctgtttgta tctgacaga ttg aac aag agg tgc ctt gag ttt ggt gaa gtt 172
Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val
1 5 10

tgt aac ttt ttt ttc cca acc tgc tgc ggc tat tgc gtt ctt ctt gtc 220
Cys Asn Phe Phe Phe Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val
15 20 25

tgc cta taaaactacc gtgatgtctt ctcttcccct ctagtagtag taggcggccg 276
Cys Leu

ctctagaagga tccaagctta cgtacgcgtg catgcgacgt catagctctt ctatagtgtc 336

acctaaattc aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt 396

tacccaactt aatcgccttg cagcacatcc cccttttcgcc agctggcgta atagcgaaga 456

ggcccgcacc gatcgccctt cccaacagtt gcgcagcctg aatggcgaat gggacgcgcc 516

ctgtagcggc gcattaag 534

<210> 104
<211> 29
<212> PRT
<213> Conus omaria

<400> 104
Leu Asn Lys Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Phe
1 5 10 15

Pro Thr Cys Cys Gly Tyr Cys Val Leu Leu Val Cys Leu
20 25

<210> 105
<211> 29
<212> PRT
<213> Conus omaria

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residues 3 and 6 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr
, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
o-Tyr

<400> 105
Cys Leu Xaa Phe Gly Xaa Val Cys Asn Phe Phe Phe Xaa Thr Cys Cys
1 5 10 15

Gly Xaa Cys Val Leu Leu Val Cys Leu
20 25

<210> 106
<211> 280
<212> DNA
<213> Conus obscurus

<220>
<221> CDS
<222> (73)..(180)

<400> 106
cgaaacatct gtccatccat ccattcgttc gttcgctgcc aaactgtaat aaataaccga 60

gtctctctgt tt gta tct gac aga tcg aaa aag caa tgc cgt caa aat ggt 111
Val Ser Asp Arg Ser Lys Lys Gln Cys Arg Gln Asn Gly
1 5 10

gaa gtg tgt gat gcg aat ttg gca cac tgc tgc agt ggc ccg tgt ttt 159
Glu Val Cys Asp Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe
15 20 25

ctc ttc tgt cta aac cag ccg tgatgtcttc tactccccgc 200
Leu Phe Cys Leu Asn Gln Pro
30 35

<210> 107
<211> 36
<212> PRT
<213> Conus obscurus

<400> 107
Val Ser Asp Arg Ser Lys Lys Gln Cys Arg Gln Asn Gly Glu Val Cys
1 5 10 15

Asp Ala Asn Leu Ala His Cys Cys Ser Gly Pro Cys Phe Leu Phe Cys
20 25 30

Leu Asn Gln Pro
35

<210> 108
<211> 32
<212> PRT
<213> Conus obscurus

<220>
<221> SITE
<222> (1)..(32)
<223> Xaa at residue 10 may be Glu or gamma-carboxy-Glu; Xaa at residue
s 23 and 32 may be Pro or hydroxy-Pro

<400> 108
Ser Lys Lys Gln Cys Arg Gln Asn Gly Xaa Val Cys Asp Ala Asn Leu
1 5 10 15

Ala His Cys Cys Ser Gly Xaa Cys Phe Leu Phe Cys Leu Asn Gln Xaa
20 25 30

<210> 109
<211> 262
<212> DNA
<213> Conus ammiralis

<220>
<221> CDS
<222> (1)..(231)

<400> 109
atg aaa ctg acg tgc gtg atg atc att gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala

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1               5                  10                  15

tgg aca ttt gcc acg gct gat gac tcc gga aat gga ttg gaa aat ctt      96
Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
            20                  25                  30

ttt tcg aag gca cat cac gaa atg aag aac ccc aaa gcc tct aaa ttg     144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
        35                  40                  45

aat aag agg tgc act caa agc ggt gaa ctt tgt gat gtg ata gac cca     192
Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro
    50                  55                  60

gac tgc tgc aat aat ttt tgc att ata ttt ttc tgc ata taaaactgcc     241
Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
65                  70                  75

gtgatgcctt ctactccccc c                                           262
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<210> 110
<211> 77
<212> PRT
<213> Conus ammiralis

<400> 110
Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala
1   5   10   15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
            20   25   30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
        35   40   45

Asn Lys Arg Cys Thr Gln Ser Gly Glu Leu Cys Asp Val Ile Asp Pro
    50   55   60

Asp Cys Cys Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
65   70   75

<210> 111
<211> 26
<212> PRT
<213> Conus ammiralis

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
      13 may be Pro or hydroxy-Pro

<400> 111
Cys Thr Gln Ser Gly Xaa Leu Cys Asp Val Ile Asp Xaa Asp Cys Cys
1   5   10   15

Asn Asn Phe Cys Ile Ile Phe Phe Cys Ile
            20   25

<210> 112
<211> 286
<212> DNA
<213> Conus textile
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<220>
<221> CDS
<222> (25)..(255)

<400> 112
ggcartaact aaaacatcac caaa atg aaa ctg acg tgc atg atg atc gtt 51
Met Lys Leu Thr Cys Met Met Ile Val
1 5

gct gtg ctg ttc ttg acc gcc tgg aca ttc gcc acg gct gat gac tcc 99
Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Ser
10 15 20 25

gga aat gga ttg gag aaa ctt ttt tcg aat gca cat cac gaa atg aag 147
Gly Asn Gly Leu Glu Lys Leu Phe Ser Asn Ala His His Glu Met Lys
30 35 40

aac ccc gaa gcc tct aat ttg aac aag agg tgc gct cct ttt ctt cac 195
Asn Pro Glu Ala Ser Asn Leu Asn Lys Arg Cys Ala Pro Phe Leu His
45 50 55

ctc tgt acc ttt ttc ttc cca aac tgc tgc aac ggc tat tgc gtt caa 243
Leu Cys Thr Phe Phe Phe Pro Asn Cys Cys Asn Gly Tyr Cys Val Gln
60 65 70

ttt atc tgc cta taaaactact gtgatgtctt ctattcccct c 286
Phe Ile Cys Leu
75

<210> 113
<211> 77
<212> PRT
<213> Conus textile

<400> 113
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
20 25 30

Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Asn Leu
35 40 45

Asn Lys Arg Cys Ala Pro Phe Leu His Leu Cys Thr Phe Phe Phe Pro
50 55 60

Asn Cys Cys Asn Gly Tyr Cys Val Gln Phe Ile Cys Leu
65 70 75

<210> 114
<211> 26
<212> PRT
<213> Conus textile

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3 and 13 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 114
Cys Ala Xaa Phe Leu His Leu Cys Thr Phe Phe Phe Xaa Asn Cys Cys

1 5 10 15

Asn Gly Xaa Cys Val Gln Phe Ile Cys Leu
20 25

<211> 115
<212> 484
<213> Conus marmoreus

<220>
<221> CDS
<222> (74)..(304)

<400> 115
ggatcctagc acagtgaatt tggcttcaca gttttccact gtcgtctttg gcatcatcca 60

aaactatcacc aag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg 109
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu
1 5 10

ttc ttg acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga 157
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
15 20 25

ttg gag aat ctt ttt tcg aag gca cat cac gaa atg aag aac ccc aaa 205
Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys
30 35 40

gac tct aaa ttg aac aag agg tgc ctt gac gct ggt gaa atg tgt gat 253
Asp Ser Lys Leu Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp
45 50 55 60

ctc ttt aat tca aaa tgc tgc agt ggg tgg tgc att att ctc ttc tgc 301
Leu Phe Asn Ser Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys
65 70 75

gca taaaactacc gtgatgtctt ctactccctt ctgtgctacc tggcttgatc 354
Ala

ttctgattggc gcgtgccctt cactggttat gaaccccccc gatccgactc tctggcggcc 414

tctgggggttc aacatccaaa taaagccgac acgatactga cgtagaaaaa aaaaaaaaaa 474

aaaaaaaaaa 484

<210> 116
<211> 77
<212> PRT
<213> Conus marmoreus

<400> 116
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Asp Ala Gly Glu Met Cys Asp Leu Phe Asn Ser
50 55 60

Lys Cys Cys Ser Gly Trp Cys Ile Ile Leu Phe Cys Ala
65 70 75

<211> 117
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 19 may be Trp or bromo-Trp

<400> 117
Cys Leu Asp Ala Gly Xaa Met Cys Asp Leu Phe Asn Ser Lys Cys Cys
1 5 10 15

Ser Gly Xaa Cys Ile Ile Leu Phe Cys Ala
20 25

<210> 118
<211> 427
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (19)..(249)

<400> 118
ttcgaaaaca tcaccaag atg aaa ctg acg agc atg atg atc gtt gct gtg 51
Met Lys Leu Thr Ser Met Met Ile Val Ala Val
1 5 10

ctg ttc ttg acc gcc tgg acg ttc gtc acg gct gac gac tcc gga aat 99
Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Gly Asn
15 20 25

gga ttg gag aat ctt ttt tcg aag gca cat cac gag atg aag aac ccc 147
Gly Leu Glu Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro
30 35 40

aaa gac tct aaa ttg aac aag agg tgc ctt gac ggt ggt gaa att tgt 195
Lys Asp Ser Lys Leu Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys
45 50 55

ggt att ttg ttt cca agc tgc tgc agt ggg tgg tgc att gtt ctc gtc 243
Gly Ile Leu Phe Pro Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val
60 65 70 75

tgt gca taaaactacc gtgatgtctt ctactcccct ctgtgctacc tgggttgatc 299
Cys Ala

ttgattggc gcgtgccctt cactggttat gaaccccact gatccgactc tctggcggcc 359

tgggggttc aacatccaaa taaagcgaca cgacaatgac aaaaaaaaaa aaaaaaaaaa 419

aaaaaaa 427

<210> 119
<211> 77
<212> PRT

<213> Conus marmoreus

<400> 119
Met Lys Leu Thr Ser Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Thr Thr Phe Val Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Lys Asp Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Asp Gly Gly Glu Ile Cys Gly Ile Leu Phe Pro
50 55 60

Ser Cys Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala
65 70 75

<210> 120
<211> 26
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1).. 26
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue 19 may be Pro or hydroxy-Pro; Xaa at residue 19 may be Trp or bromo-Trp

<400> 120
Cys Leu Asp Gly Gly Xaa Ile Cys Gly Ile Leu Phe Xaa Ser Cys Cys
1 5 10 15

Ser Gly Xaa Cys Ile Val Leu Val Cys Ala
20 25

<210> 121
<211> 470
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (70)..(303)

<400> 121
gctagcacag tgaatttggc atcacagttt tccactgtcg tattttgcat catccaaaac 60

at tac caag atg aaa ctg acg tgc atg atg atc gaa gca gag ctg ttc ttg 111
Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu
1 5 10

act gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gag 159
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu
15 20 25 30

aat ctt ttt tcg aag gca cat cac gaa atg aag aac ccc gaa gcc tct 207
Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ttg aac aag agg tgc cct aac act ggt gaa tta tgt gat gtg gtt 255
Lys Leu Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val
50 55 60

gaa caa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cct ata 303
Glu Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile
65 70 75

tagctacggt gatgtcttct actccccctct gtgctgcctg gcttgatctt tgattggcgc 363

gtggccgttca ctggttatga accccccgga tccgactctc ttgcggccta agggggttcaa 423

caaaaaaaaa aagcgacacg aaaatgaaaa aaaaaaaaaa aaaaaaa 470

<210> 122
<211> 78
<212> PRT
<213> Conus marmoreus

<400> 122
Met Lys Leu Thr Cys Met Met Ile Glu Ala Glu Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Ala Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
50 55 60

Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Pro Ile
65 70 75

<210> 123
<211> 47
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residues 2 and 26 may be Pro or hydroxy-Pro; Xaa at residues 6 and 12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 123
Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Xaa Ile
20 25

<210> 124
<211> 470
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (67)..(312)

<400> 124
ttgaaaggtg aatttcgctt atatttttct actgtcgtct ttggcatcat ccaaaacatc 60

acctaag atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg 108

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu
1 5 10

acc [illegible] tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta ttg 156
Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu
15 20 25 30

gag aat ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc 204
Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala
35 40 45

tct aaa tta aac gtg aga gac gac gag tgc gaa cct cct gga gat ttt 252
Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe
50 55 60

tgt ggc ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttc 300
Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe
65 70 75

ctc tgg tgc gcc taaaactgcc gtgatgtctt ctattccccc ctgtgctacc 352
Leu Trp Cys Ala
80

tggcttgatc tttgattggc gcgtgccctt cagtggttat gaacccccct gatccgactc 412

tctgtgggcc tcgggggttc aacatccaaa taagctgac aacacaataa aaaaaaaa 470

<210> 125
<211> 80
<212> PRT
<213> Conus marmoreus

<400> 125
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
65 70 75 80

Cys Ala

<210> 126
<211> 30
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at r
esidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue
s 24 and 28 may be Trp or bromo-Trp

<400> 126
Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile

1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
20 25 30

<210> 127
<211> 277
<212> DNA
<213> Conus striatus

<220>
<221> CDS
<222> (1)..(246)

<400> 127
atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg acg ttc gtc acg gct gtg cct cac tcc agc gat gca ttg gag aat 96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn
20 25 30

ctc tat ctg aag gca ctt cac gaa acg gaa aac cac gaa gcc tct aaa 144
Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
35 40 45

ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat ttt tgt ggc 192
Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
50 55 60

ttc ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttc ctc tgg 240
Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
65 70 75 80

tgc gca taaaactgcc gtgatgtctt ctcctcctct c 277
Cys Ala

<210> 128
<211> 82
<212> PRT
<213> Conus striatus

<400> 128
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
65 70 75 80

Cys Ala

<210> 129
<211> 80
<212> PRT

<213> Conus striatus

<220>
<221> SITE
<222> (1)..(20)
<223> Xaa at residues 3 and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 14 and 28 may be Trp or Bromo-Trp

<400> 129
Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
20 25 30

<210> 130
<211> 277
<212> DNA
<213> Conus ermaria

<220>
<221> CDS
<222> (1)..(210)

<400> 130
atg aaa ctg acg tgc gtg atg att att gct gtg ctg ttt ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg acg ttc gtc acg gct gtg cct cac tcc agc aat gca ttg gaa aat 96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

ctc tat ctg aag gca cgt cac gaa atg gaa aac ccc gaa gcc tct aaa 144
Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

ttg aac acg aga gac gac gat tgc gaa cct cct gga aat ttt tgt ggc 192
Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
50 55 60

att aca aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc 240
Ile Thr Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80

tgc gcc taaaactggc gtgatgtctt ctcctccctc c 277
Cys Ala

<210> 131
<211> 82
<212> PRT
<213> Conus ermaria

<400> 131
Met Lys Leu Thr Cys Val Met Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

```
Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
                    55                  60

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65                  70                  75                  80

Cys Ala

<210>  144
<211>  30
<212>  PRT
<213>  Conus omaria

<220>
<221>  SITE
<222>  (1..(30.
<223>  Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues
       6, 7, 15 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may
       be Trp or bromo-Trp

<400>  142
Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
1               5                  10                  15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
            20                  25                  30

<210>  143
<211>  177
<212>  DNA
<213>  Conus aulicus

<220>
<221>  CDS
<222>  (1)..(246)

<400>  143
atg aaa ctg acg tgc ctg atg ata gtt gct gtg ctg ttc ttg acc gcc      48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gca ttg gag aat      96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
            20                  25                  30

ctt tat ctg aag gca cgt cac gaa atg gaa aac ccc gaa gcc tct aaa     144
Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
        35                  40                  45

aac aat acg aga gac tac gat tgc gaa cct cct gga aat ttt tgt ggc     192
Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
    50                  55                  60

atc ata aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc     240
Ile Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65                  70                  75                  80

tgc gcc taaaactgcc gtgatgtctt ctcctccact c                         277
Cys Ala

<210>  144
<211>  80
<212>  PRT
<213>  Conus aulicus
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<400> 134
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
35 40 45

Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
50 55 60

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
65 70 75 80

Cys Ala

<210> 135
<211> 30
<212> PRT
<213> Conus aulicus

<220>
<221> SITE
<222> (1 .. 30)
<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 may be Glu or
gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or
hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Try

<400> 135
Asp Xaa Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
20 25 30

<210> 136
<211> 245
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (111)..(212)

<400> 136
ggtcgacatc atcattatta tcgatccatc tgttccatcca tctattcatt cattcgtggc 60

caaactgtaa taaataatgc aagtctctct ttctgtttgt atctgacaga ttg aac 116
Leu Asn
1

acg aga gac gac gat tgc gaa cct cct gga aat ttt tgt ggc atg ata 164
Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly Met Ile
5 10 15

aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc tgc gcc 212
Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala Cys Ala
20 25 30

taaaactgcc gtgatgtctt ctcttccgct ctagtagtag taggcggccg ctctagagga 272

tccaagctta cgtacgcgtg catgcgacgt catagctctt ctatagtgtc acctaaattc 332

aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt tacccaactt 392

aatcgccttg cagcacatcc cccttttcgcc agctggcgta atagcgaaga ggcccgcacc 452

gatcgccctt cccaacagtt gcgcagcctg aatggcgaat gggacgcgcc ctgtagcggc 512

gcattaagcg cggcgggtgt ggtggttacg cgcagcgtga ccgctacact tgccagc 572

gccctagcgc ccgctccttt cgctttcttc ccttcctttct cgccacgttc gccggctttt 632

ccccgtcaag ctctaaatcgg gggctccttt agggttccgat ttaagtgctt tac 685

<211> 157
<212> 34
<212> PRT
<213> Conus marmoreus

<400> 137
Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
1 5 10 15

Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
20 25 30

Cys Ala

<211> 138
<212> 30
<212> PRT
<213> Conus marmoreus

<220>
<221> MISC_FEATURE
<222> (1)..(30)
<223> Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 11 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

<400> 138
Asp Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
20 25 30

<210> 139
<211> 116
<212> DNA
<213> Conus regius

<220>
<221> CDS
<222> (1)..(96)

<400> 139
ttg aac cag aga gac tgc ctt agt aaa aac gct ttc tgt gcc tgg ccg 48
Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro
1 5 10 15

att ctt gga cca ctg tgc tgc agt ggc tgg tgc tta tac gtc tgc atg 96
Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
20 25 30

taaaactgcc gtgatgtctt ctatcccctc 126

<21 > 140
<211> 32
<212> PRT
<213> Conus regius

<400> 140
Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro
1 5 10 15

Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
20 25 30

<210> 141
<211> 28
<212> PRT
<213> Conus regius

<220>
<221> SITE
<222> (11)..(28)
<223> Xaa at residues 11 and 21 may be Trp or bromo-Trp; Xaa at residue
s 10 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be T
yr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
pho-Tyr

<400> 141
Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa
1 5 10 15

Leu Cys Cys Ser Gly Xaa Cys Leu Xaa Val Cys Met
20 25

<210> 142
<211> 133
<212> DNA
<213> Conus radiatus

<220>
<221> CDS
<222> (2...103)

<400> 142
a ttg aat aag aaa ggt gat gac tgc ctt gct gtt aaa aaa aat tgt ggc 49
Leu Asn Lys Lys Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly
1 5 10 15

ttt cca aaa ctt gga ggg cca tgc tgc agt ggc ttg tgc ttt ttc gtc 97
Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val
20 25 30

t gc gcc taaaactgcc gtgatgtctt ctatccccct 133
Cys Ala

<210> 143
<211> 34
<212> PRT
<213> Conus radiatus

<400> 143
Leu Asn Lys Lys Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly
1 5 10 15

Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val
20 25 30

Cys Xaa

<...> 144
<...> 70
<...> PRT
<...> Conus radiatus

<...>
<...> SITE
<...> (1)..(30)
<...> Xaa at residues 14 and 19 may be Pro or hydroxy-Pro.

<...> 144
Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly Phe Xaa Lys Leu
1 5 10 15

Gly Gly Xaa Cys Cys Ser Gly Leu Cys Phe Phe Val Cys Ala
20 25 30

<...> 145
<...> 127
<...> DNA
<...> Conus regius

<...>
<...> CDS
<...> (1)..(96)

<...> 145
Trp Asn Gln Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro
1 5 10 15

Gln Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
20 25 30

<...> 127

<...> 146
<...> 32
<...> PRT
<...> Conus regius

<...> 146
Trp Asn Gln Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro
1 5 10 15

Gln Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
20 25 30

<...> 147
<...> 32
<...> PRT
<...> Conus regius

<...>
<...> SITE
<...> (1)..(28)
<...> Xaa at residues 4 and 12 may be Pro or hydroxy-Pro.

<400> 147
Asp Cys Leu Xaa Arg Asp Thr Phe Cys Ala Leu Xaa Gln Leu Gly Leu
1 5 10 15

Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
20 25

<210> 148
<211> 345
<212> DNA
<213> Conus aurisiacus

<220>
<221> CDS
<222> (1)..(234)

<400> 148
atg aaa ctg acg tgc gtg atg acc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ctg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aat aag aga gat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192
Asn Lys Arg Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
50 55 60

gga ggt ctc tgc tgc agc gag att tgc att gtt tgg tgc aca 234
Gly Gly Leu Cys Cys Ser Glu Ile Cys Ile Val Trp Cys Thr
65 70 75

tgagtcgtat tctgctggta catttgtggg cttcaacgga ggactctgct gcagcaacct 294

ctgcttattt ctcgtgcggct ttaatatatt c gtgatgtctt ctactccaat c 345

<210> 149
<211> 78
<212> PRT
<213> Conus aurisiacus

<400> 149
Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
50 55 60

Gly Gly Leu Cys Cys Ser Glu Ile Cys Ile Val Trp Cys Thr
65 70 75

<210> 150
<211> 27

<212> PRT
<213> Conus aurisiacus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 ma
y be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or br
om-Trp

<400> 150
Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Ile Cys Ile Val Xaa Cys Thr
20 25

<210> 151
<211> 412
<212> DNA
<213> Conus purpurascens

<220>
<221> CDS
<222> (1)...(243)

<400> 151
atg aaa ttg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg gca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
Trp Ala Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

gat aaa aag gaa gcc tgc tat gcg cct ggt act ttt tgt ggc ata aag 192
Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

ggc gag gca tgc tgc agt gag ttt tgt ctc ccg ggc gtc tgc ttc ggt 240
Gly Glu Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
65 70 75 80

ggt taactgccgt gatgtcttct actccctct gtgctacctg gcttgatctt 293
Gly

gatctggcgt gtgccattca ctggttatga accactgat cttacctctc ttgaaggacc 353

ctgggatcc agcatccaaa taagcgacat cccaatgaaa aaaaaaaaaa aaaaaaaaa 412

<210> 152
<211> 80
<212> PRT
<213> Conus purpurascens

<400> 152
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

Pro Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
65 70 75 80

Gly

<210> 153
<211> 29
<212> PRT
<213> Conus purpurascens

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 153
Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

<210> 154
<211> 29
<212> PRT
<213> Conus purpurascens

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 154
Xaa Ala Cys Xaa Ala Xaa Gly Thr Ala Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

<210> 155
<211> 29
<212> PRT
<213> Conus purpurascens

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su

lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
o or hydroxy-Pro

<400> 156
Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ala Lys Xaa Gly Leu
1 5 10 15

Cys Lys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

<210> 156
<211> 28
<212> PRT
<213> Genus purpurascens

<220>
<221> SITE
<222> (1)..(28)
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
residues 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
o or hydroxy-Pro

<400> 156
Xaa Ala Cys Xaa Ala Xaa Gly Ala Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Lys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
20 25

<210> 157
<211> 249
<212> DNA
<213> Genus magus

<220>
<221> CDS
<222> (1)..(252)

<400> 157
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc acc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

ttc ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg 144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag aga gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt 192
Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
50 55 60

ttc ggc ccc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt 240
Phe Gly Pro Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

ttc gat tct tgg taacagtgtg cgttggttag tgtcttctcc tcgcctc 289
Phe Asp Ser Gly

<210> 158

<211> 84
<212> PRT
<213> Conus magus

<400> 15
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
50 55 60

Phe Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

Val Asp Ser Gly

<210> 16
<211> 84
<212> PRT
<213> Conus magus

<220>
<221> SITE
<222> (4)..(84)
<223> Xaa at residue 4 may be Tyr, 3,5-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
Xaa at residue 25 may be Trp or bromo-Trp

<400> 16
Asp Gly Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser
20 25 30

<210> 160
<211> 253
<212> DNA
<213> Conus magus

<220>
<221> CDS
<222> (1)..(249)

<400> 160
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc acc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg 144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag aga gat gaa tgc tat cct cct ggt aca ttt tgt ggc atc aaa 192
Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

cca aga ctt tgc tgc agc gcg ata tgc tta tcg ttt gtc tgc ata tca 240
Pro Arg Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
65 70 75 80

ttt gat ttt tgattgatgt cttctcctcc cctc 273
Phe Asp Phe

<210> 161
<211> 83
<212> PRT
<213> Conus magus

<400> 161
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

Thr Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

Pro Arg Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
65 70 75 80

Phe Asp Phe

<210> 162
<211> 30
<212> PRT
<213> Conus magus

<220>
<221> SITE
<222> (1)..(32)
<223> Xaa at residue 2 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6and 14 may be Pro or hydroxy-Pro

<400> 162
Asp Xaa Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Xaa Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe
20 25 30

<210> 163
<211> 83
<212> DNA
<213> Conus magus

<220>
<221> CDS
<222> (1)..(252)

<400> 163
atg aaa ctg acg tgc gtg atg atc gtt gct gta ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg acg ttc gtc acg gct gat gac tcc aga tat gga ctg aag gat ctg 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
20 25 30

ttt ccg aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac cag aga gaa gcc tgc tat aat ggt ggt tca ttt tgt ggc atc cat 192
Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Ser Phe Cys Gly Ile His
50 55 60

cca gga ctc tgc tgc tcc agc gag ttc tgc att ctt tgg tgc atc acg ttt 240
Pro Gly Leu Cys Cys Ser Glu Phe Cys Ile Leu Trp Cys Ile Thr Phe
65 70 75 80

gtt gat tct ggc taactgtgtg cgttggttga tgtcttctcc tcccatc 289
Val Asp Ser Gly

<210> 164
<211> 84
<212> PRT
<213> Conus magus

<400> 164
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
20 25 30

Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Ser Phe Cys Gly Ile His
50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Ile Leu Trp Cys Ile Thr Phe
65 70 75 80

Val Asp Ser Gly

<210> 165
<211> 42
<212> PRT
<213> Conus magus

<220>
<221> SITE
<222> (1)..(34)
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 11 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or bromo-Trp

<400> 165
Xaa Ala Cys Xaa Asn Ala Gly Ser Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Ile Leu Xaa Cys Ile Thr Phe Val Asp Ser
20 25 30

<210> 166
<211> 271
<212> DNA
<213> Conus magus

<220>
<221> CDS
<222> (1)..(249)

<400> 166
atg aaa ctg acg tgc atg atg atc gtt gct gta ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg act ttc gtc acg gct gat gac tcc aga tat gga ctg aag gat ctg 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
20 25 30

ttc cct aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aat caa aga gaa gcc tgc tat aat gct ggt aca ttt tgt ggc atc aaa 192
Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys
50 55 60

cca gga ctt tgc tgc agc gcg ata tgc tta tcg ttt gtc tgc ata tca 240
Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
65 70 75 80

ttt gat ttg attgatgtct tctcctcccc tc 271
Phe Asp Leu

<210> 167
<211> 83
<212> PRT
<213> Conus magus

<400> 167
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu
20 25 30

Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys
50 55 60

Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
65 70 75 80

Phe Asp Leu

<210> 168
<211> 83
<212> PRT
<213> Conus magus

<220>
<221> SITE
<222> (1)..(32)
<223> Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro

<400> 168
Xaa Ala Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe
20 25 30

<210> 169
<211> 972
<212> DNA
<213> Conus ermineus

<220>
<221> CDS
<222> (1)..(243)

<400> 169
atg aaa ctt acg tgc gtg atg atc gtt gct gtg ctg ttc ctg act gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag 192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

ggc gga ctg tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240
Gly Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65 70 75 80

tgt taactccgc gatgtcttct cctccgctc 272
Cys

<210> 170
<211> 81
<212> PRT
<213> Conus ermineus

<400> 170
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65 70 75 80

Gly

<...> 171
<...> AA
<...> PRT
<...> Conus ermineus

<...>
<...> SITE
<...> (1)..(24)
<...> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 171
Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
20 25

<...> 172
<...> 171
<...> DNA
<...> Conus purpurascens

<...>
<...> CDS
<...> (1)..(243)

<400> 172
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg act gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg 144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

gat aaa aag gaa gcc tgc tat ccg ccc ggt act ttt tgt ggc ata aag 192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

ccg ggt cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt 240
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65 70 75 80

tga taactgccgt gatgtcttct cctcccctc 272
***

<...> 173
<...> 81
<...> PRT
<...> Conus purpurascens

<400> 173

Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
20 25 30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
35 40 45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65 70 75 80

Gly

(10) 173
(11) 24
(12) PRT
(13) Conus purpurascens

(220)
(221) SITE
(222) (1)..(24)
(223) Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 14 and 24 may be Pro or hydroxy-Pro

(400) 174
Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
20 25

(210) 175
(211) 166
(212) DNA
(213) Conus striatus

(220)
(221) CDS
(222) (1)..(140)

(400) 175
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc act 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

ttc tgg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Trp Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aat aaa aga gaa ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cat 192
Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
50 55 60

cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240

Pr Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

266

at gat tgatgtcttc tcctcccctc
Ile Asp

<(1)> 176
<(11)> 82
<(12)> PRT
<(13)> Conus striatus

<(400)> 176
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

Pro Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

Ile Asp

<(210)> 177
<(211)> 91
<(212)> PRT
<(213)> Conus striatus

<(220)>
<(221)> SITE
<(222)> (1)..(91)
<(223)> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or bromo-Trp

<(400)> 177
Xaa Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
20 25 30

<(210)> 178
<(211)> 266
<(212)> DNA
<(213)> Conus striatus

<(220)>
<(221)> CDS
<(222)> (1)..(246)

<(400)> 178
atg aaa ctt acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc act 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat ggg ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu

20 25 30

ttt ctg aaq gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aaa agg gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cat 192
Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
50 55 60

cca gga ctt tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt 240
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

att gat tgatgtcttc tcctcccctc 266
Ile Asp

(210) 179
(211) 82
(212) PRT
(213) Conus striatus

(400) 179
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

Pro Lys Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

Ile Asp

(210) 180
(211) 31
(212) PRT
(213) Conus striatus

(220)
(221) SITE
(222) (1)..(31)
(223) Xaa at residue 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Trp or bromo-Trp

(400) 180
Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Lys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
20 25 30

(210) 181
(211) 81
(212) PRT
(213) Conus striolatus

<2..>
<2..1 SITE
<2..2 (1)..(21)
<2..3 Xaa at residues 6 and 14 may be Pro or hydroxy-Pro; Xaa at residu
       e 31may be Glu or gamma-carboxy-Glu

<4.. 191
Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1   5   10   15

Cys Tyr Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa
            20   25   30

<21.. 162
<21.. 945
<21.. DNA
<21.. Canus Catus

<22..
<22..1 CDS
<22..2 (1)..(234)

<40.. 192
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1   5   10   15

tgg acg ttc gtc acg gct gat gac tcc aga aat gga ctg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
            20   25   30

ttt ccc aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35   40   45

aat aaa aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192
Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
    50   55   60

cca gga ctc tgc tgc agc gag ctt tgc ctg gtt tgg tgc act   234
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr
65   70   75

<400> gtatgctat tcttctgtga catttttgtgg cttcaacgga ggactctgct gcagcaacct 294

<400> cttcatttt tcgtgtgcct aacatttcgt gatgtcttct ctattcccct c 345

<210> 183
<211> 78
<212> PRT
<213> Canus catus

<400> 183
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1   5   10   15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
            20   25   30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35   40   45

Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
    50   55   60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr
65 70 75

<400> 184
<211> 27
<212> PRT
<213> Conus catus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
hydroxy-Pro; Xaa at residue 24 may be Glu or gamma-carboxy-Glu;
Xaa at residue 25 may be Trp or bromo-Trp

<400> 184
Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Val Xaa Cys Thr
20 25

<210> 185
<211> 345
<212> DNA
<213> Conus catus

<220>
<221> CDS
<222> (1)..(234)

<400> 185
atg aaa ctg agg tgt atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ctg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac aag aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat 192
Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
50 55 60

tgc gga ctc tgc tgc agc gag ctt tgc ctg ggt tgg tgc aca 234
Cys Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr
65 70 75

tgagtgctat tctactggta cattttgtgg cttcaacgga ggactctgct gcagcaacct 294

ttgttattt tcgtgtgctt aacatttcgt gatgtcttct ctattccccc c 345

<210> 186
<211> 78
<212> PRT
<213> Conus catus

<400> 186
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
50 55 60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr
65 70 75

<210> 187
<211> 27
<212> PRT
<213> Conus ratus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
Xaa at residue 25 may be Trp or bromo-Trp

<400> 187
Xaa Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Gly Xaa Cys Thr
20 25

<210> 188
<211> 266
<212> DNA
<213> Conus distans

<220>
<221> CDS
<222> (1)..(246)

<400> 188
atg aaa ctg acg tgt ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctc 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

tct ccg aag gca cct cac gaa atg aag aac ccc gaa gcc tct aaa tcg 144
Ser Pro Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

aat aaa aga tat gag tgc tat cta ctg gta cat ttt tgt ggc atc aac 192
Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn
50 55 60

gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

266

ttt tcg tgatgtcttc tcctcccatc
Phe Ser

<2[illegible]> 189
<211> 32
<212> PRT
<213> Conus distans

<400> 189
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Ser Pro Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn
50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Phe Ser

<210> 190
<211> 31
<212> PRT
<213> Conus distans

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 190
Xaa Xaa Cys Xaa Leu Leu Val His Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

<210> 191
<211> 113
<212> DNA
<213> Conus regius

<220>
<221> CDS
<222> (1)..(93)

<400> 191
ttg agc aag aga gac tgc ctt cct gac tac acg att tgt gcc ttc aat 48
Leu Ser Lys Arg Asp Cys Leu Pro Asp Tyr Thr Ile Cys Ala Phe Asn
1 5 10 15

atg ggt ctg tgc tgc agc gac aag tgc atg ctc gtc tgc ctg ccg 93
Met Gly Leu Cys Cys Ser Asp Lys Cys Met Leu Val Cys Leu Pro
20 25 30

tgatgtcttc tcctcccctc 113

<210> 192
<211> 31
<212> PRT
<213> Cynus regius

<400> 142
Leu Asp Lys Arg Asp Cys Leu Pro Asp Tyr Thr Ile Cys Ala Phe Asn
1 5 10 15

Met Gly Leu Cys Cys Ser Asp Lys Cys Met Leu Val Cys Leu Pro
20 25 30

<210> 193
<211> 27
<212> PRT
<213> Cynus regius

<220>
<221> MISC_FEATURE
<222> (1)..(27)
<223> Xaa at residues 5 and 27 may be Pro or hydroxy-Pro; Xaa at residu
e 9 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T
yr or O-phospho-Tyr

<400> 193
Asp Cys Leu Xaa Asp Xaa Thr Ile Cys Ala Phe Asn Met Gly Leu Cys
1 5 10 15

Cys Ser Asp Lys Cys Met Leu Val Cys Leu Xaa
20 25

<210> 194
<211> 116
<212> DNA
<213> Cynus regius

<220>
<221> CDS
<222> (1)..(96)

<400> 194
ttg aac aag aga atc atc tgc ttt cct gac tac atg ttt tgt ggc gtc 48
Leu Asn Lys Arg Ile Ile Cys Phe Pro Asp Tyr Met Phe Cys Gly Val
1 5 10 15

aac gtg ttt ctg tgc tgc agt ggc aac tgc ctt ctc atc tgc gtg ccg 96
Asn Val Phe Leu Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Pro
20 25 30

tgaatgctgc tactcgccta 116

<210> 195
<211> 32
<212> PRT
<213> Cynus regius

<400> 195
Leu Asn Lys Arg Ile Ile Cys Phe Pro Asp Tyr Met Phe Cys Gly Val
1 5 10 15

Asn Val Phe Leu Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Pro
20 25 30

<210> 196

<211> 38
<212> PRT
<213> Conus regius

<220>
<221> MISC_FEATURE
<222> (1)..(28)
<223> Xaa at residues 5 and 28 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 196
Ile Ile Cys Gly Xaa Asp Xaa Met Phe Cys Gly Val Asn Val Phe Leu
1 5 10 15

Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Xaa
20 25

<210> 197
<211> 259
<212> DNA
<213> Conus gloriamaris

<220>
<221> CDS
<222> (1)..(228)

<400> 197
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gcg ttg gag aat 96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

ctt tat ctg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa 144
Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
35 40 45

ttg aac aag agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac 192
Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
50 55 60

taa tgc tgc agt ggc tgg tgc att ttc gcc tgc ctc taaaactgtc 238
Xaa Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu
65 70 75

gtgatgcctt ctgctccct c 259

<210> 198
<211> 76
<212> PRT
<213> Conus gloriamaris

<400> 198
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu
65 70 75

<210> 198
<211> 24
<212> PRT
<213> Conus gloriamaris

<220>
<221> SITE
<222> (1)..(24)
<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or nitro-Trp

<400> 198
Cys Xaa Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser
1 5 10 15

Gly Xaa Cys Ile Phe Ala Cys Leu
20

<210> 199
<211> 288
<212> DNA
<213> Conus dalli

<220>
<221> CDS
<222> (1)..(228)

<400> 199
atg aaa ttg acg tgc att atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Ile Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gcg ttg gag aat 96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

ctt tat ctg aag gca cat cat gaa atg aac aac ccc gag gac tct gaa 144
Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
35 40 45

tta aac aag agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac 192
Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
50 55 60

tta tgt tgc agt ggc tgg tgc att ttc gtc tgc ctc taaaactgcc 238
Leu Cys Cys Ser Gly Trp Cys Ile Phe Val Cys Leu
65 70 75

ttatgtttt ctcttccatc 258

<210> 201
<211> 76
<212> PRT
<213> Conus dalli

<400> 201
Met Lys Leu Thr Cys Ile Met Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Cys Leu
65 70 75

<210> 232
<211> 34
<212> PRT
<213> Conus dalli

<220>
<221> SITE
<222> (1)..(34)
<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
bromo-Trp

<400> 232
Cys Xaa Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn Gln Cys Cys Ser
1 5 10 15

Gly Xaa Cys Ile Phe Val Cys Leu
20

<210> 233
<211> 259
<212> DNA
<213> Conus pennaceus

<220>
<221> CDS
<222> (21)..(228)

<400> 233
atg aaa ttg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca gtc gtc acg gct gtg cct cac tcc aac aag cgg ttg gcg aat 96
Trp Thr Val Val Thr Ala Val Pro His Ser Asn Lys Arg Leu Ala Asn
20 25 30

ctt tat ctg aag gca cgt cac gaa atg aaa aac ccc gaa gcc tct aat 144
Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn
35 40 45

gtg gac aag agg tgc ttt gag agt tgg gta gct tgt gag tct cca aaa 192
Val Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys
50 55 60

cga tgc tgc agt cac gtg tgc ctt ttc gtc tgc acc tgaaactgcc 238
Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr
65 70 75

gtgatgtctt ctctccccct c 259

<210> 204
<211> 76
<212> PRT
<213> Conus pennaceus

<400> 204
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Val Val Thr Ala Val Pro His Ser Asn Lys Arg Leu Ala Asn
20 25 30

Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn
35 40 45

Val Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys
50 55 60

Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr
65 70 75

<210> 205
<211> 24
<212> PRT
<213> Conus pennaceus

<220>
<221> SITE
<222> (1)..(24)
<223> Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 5 may be Trp or bromo-Trp; Xaa at residue 11 may be Pro o
r hydroxy-Pro

<400> 205
Cys Phe Xaa Ser Xaa Val Ala Cys Xaa Ser Xaa Lys Arg Cys Cys Ser
1 5 10 15

His Val Cys Leu Phe Val Cys Thr
20

<210> 206
<211> 228
<212> DNA
<213> Conus distans

<220>
<221> CDS
<222> (1)..(228)

<400> 206
atg aaa ctg acg tgt atg ttg atc atc gct gtg ctg ttc ctg acg gcc 48
Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgt caa ctc tct aca aat gcg agt tac gcc aga agt aag cag aag cat 96
Cys Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His
20 25 30

cgt gtt ctg agg tcg act gac aaa aac tcc aag ttg acc cag cgt tgc 144
Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys
35 40 45

aat gaa gct caa gaa cat tgc act caa aat cct gac tgc tgc agt gag 192
Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu

50 55 60

tct tgc aat aag ttt gtc ggc aga tgc ttg tca gac tgatctgatg 238
Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
65 70 75

tgtgctcctc ccatc 253

<210> 207
<211> 76
<212> PRT
<213> Conus distans

<400> 207
Met Lys Leu Thr Cys Met Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His
20 25 30

Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys
35 40 45

Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu
50 55 60

Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
65 70 75

<210> 208
<211> 29
<212> PRT
<213> Conus distans

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 3, 6 and 17 may be Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Pro or hydroxy-Pro

<400> 208
Cys Asn Xaa Ala Gln Xaa His Cys Thr Gln Asn Xaa Asp Cys Cys Ser
1 5 10 15

Xaa Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
20 25

<210> 209
<211> 59
<212> DNA
<213> Conus ammiralis

<220>
<221> CDS
<222> (1)..(228)

atg aaa ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gtg ccc gac tcc agc aat gcg ttg gag aat 96
Trp Thr Phe Val Thr Ala Val Pro Asp Ser Ser Asn Ala Leu Glu Asn
20 25 30

ctt tat ctg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa 144
Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
35 40 45

ttg aac aag agg tgc tat gat ggt ggg aca agt tgt aac act gga aac 192
Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn
50 55 60

caa tgc tgc agt ggc tgg tgc att ttc ctc tgc ctc taaaactgcc 238
Gln Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu
65 70 75

gtgatgtctt cttcccct c 259

<210> 210
<211> 76
<212> PRT
<213> Conus ammiralis

<400> 210
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro Asp Ser Ser Asn Ala Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
35 40 45

Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn
50 55 60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu
65 70 75

<210> 211
<211> 24
<212> PRT
<213> Conus ammiralis

<220>
<221> SITE
<222> (1)..(24)
<223> Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
bromo-Trp

<400> 211
Cys Xaa Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
1 5 10 15

Gly Xaa Cys Ile Phe Leu Cys Leu
20

<210> 212
<211> 286
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (25)..(255)

<400> 212

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ggcattacct aaaacatcac caag atg aaa ctg acg tgc atg atg atc gtt          51
                           Met Lys Leu Thr Cys Met Met Ile Val
                           1               5

gct gtg ctg ttc ttg acc gcc tgg aca ttc gtc acg gct gcg cct cac          99
Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Thr Ala Ala Pro His
10                  15                  20                  25

tcc agc aat gcg ttg gag aat ctt tat ctg aag gca cat cat gaa atg         147
Ser Ser Asn Ala Leu Glu Asn Leu Tyr Leu Lys Ala His His Glu Met
                30                  35                  40

aac aac ccc gaa gcc tct gaa ttg aac aag agg tgc tat gat agt ggg         195
Asn Asn Pro Glu Ala Ser Glu Leu Asn Lys Arg Cys Tyr Asp Ser Gly
            45                  50                  55

aca agt tgt aac act gga aac caa tgc tgc agt ggc tgg tgc att ttc         243
Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp Cys Ile Phe
        60                  65                  70

gtc tct tgc ctc taaaactacc gtgatgtctt ctcctccact c                     286
Val Ser Cys Leu
    75

<210>  213
<211>  77
<212>  PRT
<213>  Conus textile

<400>  213
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

Trp Thr Phe Val Thr Ala Ala Pro His Ser Ser Asn Ala Leu Glu Asn
            20                  25                  30

Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Ala Ser Glu
        35                  40                  45

Leu Asn Lys Arg Cys Tyr Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn
    50                  55                  60

Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Ser Cys Leu
65                  70                  75

<210>  214
<211>  35
<212>  PRT
<213>  Conus textile

<220>
<221>  SITE
<222>  (1)..(25)
<223>  Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
       r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
       bromo-Trp

<400>  214
Cys Xaa Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
1               5                  10                  15

Gly Xaa Cys Ile Phe Val Ser Cys Leu
            20                  25
```

<210> 215
<211> 272
<212> DNA
<213> Conus gloriamaris

<220>
<221> CDS
<222> (1)..(252)

<400> 215
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ctg aca gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat ctt 96
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

ttt tcg aaa tca cgt gac gaa atg gag gac ccc gaa gct tct aaa ttg 144
Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
35 40 45

gag aaa agg gat tgc caa gca cta tgg gat tat tgt cca gta ccg ctc 192
Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu
50 55 60

ttg tca tcg ggt gat tgc tgc tat ggc tta atc tgt ggc cct ttc gtc 240
Leu Ser Ser Gly Asp Cys Cys Tyr Gly Leu Ile Cys Gly Pro Phe Val
65 70 75 80

tgc att gga tgg tgatgtcttc tactccgatc 272
Cys Ile Gly Trp

<210> 216
<211> 84
<212> PRT
<213> Conus gloriamaris

<400> 216
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
35 40 45

Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu
50 55 60

Leu Ser Ser Gly Asp Cys Cys Tyr Gly Leu Ile Cys Gly Pro Phe Val
65 70 75 80

Cys Ile Gly Trp

<210> 217
<211> 33
<212> PRT
<213> Conus gloriamaris

<220>
<221> SITE
<222> (1)..(33)

<223> Xaa at residues 6 and 33 may be Trp or bromo-Trp; Xaa at residues 8 and 21 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 27 may be Pro or hydroxy-Pro

<400> 217
Asp Cys Gln Ala Leu Xaa Asp Xaa Cys Xaa Val Xaa Leu Leu Ser Ser
1 5 10 15

Gly Asp Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Ile Gly
20 25 30

Xaa

<210> 218
<211> 275
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (1)..(249)

<400> 218
atg aaa ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc atg gct gat gac tcc aac aat gga ctg gca aat ctt 96
Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

ttc tcg aaa tca cgt gac gaa atg gag gat acc gat cct tct aaa ttg 144
Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Thr Asp Pro Ser Lys Leu
35 40 45

gag aac aga aaa act tgc caa aga agg tgg gat ttt tgt cca gga tcg 192
Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser
50 55 60

ctc gtt gga gtg ata act tgc tgc ggt ggc tta atc tgt ttt ctg ttc 240
Leu Val Gly Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe
65 70 75 80

ttc tgc gtt tgatagtgat gctcttctcc tcccct 275
Phe Cys Val

<210> 219
<211> 83
<212> PRT
<213> Conus omaria

<400> 219
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Thr Asp Pro Ser Lys Leu
35 40 45

Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser
50 55 60

Leu Val Gly Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe
60 70 75 80

Phe Cys Val

<400> 220
<211> 32
<212> PRT
<213> Genus omaria

<220>
<221> SITE
<222> (1)..(32)
<223> Xaa at residue 7 may be Trp or bromo-Trp; Xaa at residue 10 may b
e Pro or hydroxy-Pro

<400> 220
Lys Thr Cys Gln Arg Arg Xaa Asp Phe Cys Xaa Gly Ser Leu Val Gly
1 5 10 15

Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe Phe Cys Val
20 25 30

<210> 221
<211> 276
<212> DNA
<213> Genus dalli

<220>
<221> CDS
<222> (1)..(246)

<400> 221
atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ctg aca gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat ctt 96
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

ttt tcg aaa tta cgt gac gaa atg gag gac ccc gaa ggt tct aaa ttg 144
Phe Ser Lys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu
35 40 45

tat aaa aag gat tgc caa gaa aaa tgg gat tat tgt cca gta ccg ttc 192
Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe
50 55 60

tta gga tcg agg tat tgc tgc gat ggc ttt atc tgt cca tct ttc ttc 240
Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe
65 70 75 80

tgc gct tgatagtgat gtattcncta ttcccctc 274
Cys Ala

<210> 222
<211> 82
<212> PRT
<213> Genus dalli

<400> 222
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
20 25 30

Pro Ser Lys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu
35 40 45

Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe
50 55 60

Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe
65 70 75 80

Cys Ala

<210> 13
<211> 31
<212> PRT
<213> Conus dalli

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residues 8 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 26 may be Pro or hydroxy-Pro

<400> 13
Asp Cys Gln Xaa Lys Xaa Asp Xaa Cys Xaa Val Xaa Phe Leu Gly Ser
1 5 10 15

Arg Xaa Cys Cys Asp Gly Phe Ile Cys Xaa Ser Phe Phe Cys Ala
20 25 30

<210> 14
<211> 271
<212> DNA
<213> Conus dalli

<220>
<221> CDS
<222> (1)..(252)

<400> 14
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ttg ttc ctg aca gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat cat 96
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His
20 25 30

ttt tgg aaa tca cgt gac gaa atg gag gac cct gaa gct tct aaa ttg 144
Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
35 40 45

gag aaa agg gat tgc caa ggc gaa tgg gag ttt tgt ata gta ccg gtc 192
Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val
50 55 60

ctt gga ttt gtg tat tgc tgc ccc tgg ctt atc tgt ggc cct ttc gtc 240
Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
65 70 75 80

tgc gtt gat atc tgatgtcttc tatccccctc 271
Cys Val Asp Ile

<400> 225
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His
20 25 30

Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
35 40 45

Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val
50 55 60

Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
65 70 75 80

Cys Val Asp Ile

<210> 226
<211> 33
<212> PRT
<213> Genus dalli

<220>
<221> SITE
<222> (1)..(33)
<223> Xaa at residues 5 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r
esidues 6 and 22 may be Trp or bromo-Trp; Xaa at residues 12, 21
and 27 may be Pro or hydroxy-Pro;

<220>
<221> SITE
<222> (1)..(33)
<223> Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-T
yr, O-sulpho-Tyr or O-phospho-Tyr

<400> 226
Asp Cys Gln Gly Xaa Xaa Xaa Phe Cys Ile Val Xaa Val Leu Gly Phe
1 5 10 15

Val Xaa Cys Cys Xaa Xaa Leu Ile Cys Gly Xaa Phe Val Cys Val Asp
20 25 30

Ile

<210> 227
<211> 265
<212> DNA
<213> Genus pennaceus

<220>
<221> CDS
<222> (1)..(234)

<400> 227
atg aaa ctg acg tgc ctg atg atc att gct gtg ctg ttc ttg acc gcc 48

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Met Lys Leu Thr Cys Leu Met Ile Ile Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg
            20                  25                  30

Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
        35                  40                  45

Glu Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys
    50                  55                  60

Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
65                  70                  75

Xaaaactgct gtgatgtctt ctcttcccat c

<210>  223
<211>  78
<212>  PRT
<213>  Conus pennaceus

<400>  223
Met Lys Leu Thr Cys Leu Met Ile Ile Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg
            20                  25                  30

Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
        35                  40                  45

Glu Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys
    50                  55                  60

Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
65                  70                  75

<210>  229
<211>  31
<212>  PRT
<213>  Conus pennaceus

<220>
<221>  SITE
<222>  (1)..(31)
<223>  Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue
       7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
       or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydrox
       y-Pro

<400>  229
Gly Cys Leu Xaa Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn
1               5                  10                  15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
            20                  25                  30

<210>  230
<211>  426
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<213> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (122)..(229)

<400> 2
tgtgacatcc atccatcatcg atccatctgt ccatccatct gtccatccat ccattcattc 60

gttgactgtc aaactgttcat aaatatttga gtctctcttt ctgtttttat ctgacagatt 120

aat gag aga gac tgc ctt aat gtt gat tat ttt tgc ggc ata ccg ttt 169
Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe
1 5 10 15

ttg aac aac ggg cta tgc tgc agt ggc aat tgt gtt ttt gtc tgc aca 217
Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr
20 25 30

ccc caa ggg aag taaaactgcc gtgatgtctt ctcttccccc ctagtagtag 269
Pro Gln Gly Lys
35

tagcggccg ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt 329

ctctagtgtc acctaaattc aattcactgg ccgtccgttt tacaacgtcg tgactgggaa 389

aaccctggcg ttacccaact taatcgcctt gcagcacat 428

<210> 231
<211> 36
<212> PRT
<213> Conus marmoreus

<400> 231
Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro Phe
1 5 10 15

Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr
20 25 30

Pro Gln Gly Lys
35

<210> 232
<211> 30
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residue 6 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 11 and 29 may b
e Pro or hydroxy-Pro

<400> 232
Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn Gly
1 5 10 15

Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
20 25 30

<210> 233
<211> 227
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (105)..(224)

<400> 233
tcgaaatcat catcatcgat ccatctgtcc atccatccat tcattcattc gctgccaaac 60

tttcataaaa atttgagtct ctctttctgt ttttatctga caga ttg gac aag aga 116
Leu Asp Lys Arg
1

agg tgc ctg gaa gct gat tat tat tgc gtc tta ccg ttt gtg ggc aac 164
Arg Cys Leu Glu Ala Asp Tyr Tyr Cys Val Leu Pro Phe Val Gly Asn
5 10 15 20

ggg atg tgc tgc agt ggc att tgt gtt ttt gtc tgc ata gcc caa cgc 212
Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg
25 30 35

ttt aaa acc gtc tga 227
Phe Lys Thr Val
40

<210> 234
<211> 40
<212> PRT
<213> Conus marmoreus

<400> 234
Leu Asp Lys Arg Glu Cys Leu Glu Ala Asp Tyr Tyr Cys Val Leu Pro
1 5 10 15

Phe Val Gly Asn Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys
20 25 30

Ile Ala Gln Arg Phe Lys Thr Val
35 40

<210> 235
<211> 36
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(36)
<223> Xaa at residues 1 and 4 may be Glu or gamma-carboxy-Glu; Xaa at r
esidues 7 and 8 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr
, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 12 may be Pro or
Hydroxy-Pro

<400> 235
Xaa Cys Leu Xaa Ala Asp Xaa Xaa Cys Val Leu Xaa Phe Val Gly Asn
1 5 10 15

Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg
20 25 30

Phe Lys Thr Val

35

<220> 236
<221> 525
<212> DNA
<213> Conus marmoreus

<400>
<221> CDS
<222> (131)..(241)

<400> 236
gtaaaggtcc ggaattcccg ggtcgacatc atcatcatcg atccatctgt ccatccatcc 60

atccattcat tcattcgctg ccaaactgtc ataaacattt gagtctctct ttctgttttt 120

atctgacaga ttg aac gag aga gac tgc ctt gaa cct gat tat gtt tgc 169
Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys
1 5 10

ggc ata ccg ttt gtg ttc aac ggg cta tgc tgc agt gga att tgt gtt 217
Gly Ile Pro Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val
15 20 25

ttt atc tgc ata gcc caa aag tat taaaacgccg tgatgtcttc tattccatc 271
Phe Ile Cys Ile Ala Gln Lys Tyr
30 35

tagtagtagt aggcggccgc tctagaggat ccaagcttac gtacgcgtgc atgcgacgtc 331

atcgactctc tatagtgtca cctaaattca attcactggc cgtcgtttta caacgtcgtg 391

actgggtaaaa ccctggcgtt acccaactta atcgccttgc agcacatccc cctttcgcca 451

gctggcgtaa tagcgaagga ggcccgcacc gatcgccctt cccaacagtt gcgcagcctg 511

aatggcgaat gggg 525

<210> 237
<211> 37
<212> PRT
<213> Conus marmoreus

<400> 237
Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys Gly Ile Pro
1 5 10 15

Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val Phe Ile Cys
20 25 30

Ile Ala Gln Lys Tyr
35

<210> 238
<211> 33
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(33)
<223> Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residues 5 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 35 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O

-phospho-Tyr

<400> 23
Asp Cys Leu Xaa Xaa Asp Xaa Val Cys Gly Ile Xaa Phe Val Phe Asn
1 5 10 15

Gly Leu Cys Cys Ser Gly Ile Cys Val Phe Ile Cys Ile Ala Gln Lys
20 25 30

Xaa

<210> 239
<211> 537
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (146)..(247)

<400> 239
gttaacgcgtg caggtaccgg tccggaattc ccgggtcgac atcatcatca tcatcgatcc 60

agctgtccat ccatctattc attcattcgc tgtccaaact g taatacatat tagaatctct 120

gtttctattt gtatctgaca gattg gag aaa agg gcg tgc agc aaa aaa tgg 172
Glu Lys Arg Ala Cys Ser Lys Lys Trp
1 5

gaa tat tgt ata gta ccg atc ctt gga ttc gta tat tgc tgc cct ggc 220
Glu Tyr Cys Ile Val Pro Ile Leu Gly Phe Val Tyr Cys Cys Pro Gly
10 15 20 25

ttg atc tgt ggt cct ttc gtc tgc gtt tgatagtgat gtcttctcct 267
Leu Ile Cys Gly Pro Phe Val Cys Val
30

cgatcttagt agtagtaggc ggccgctcta gaggatccaa gcttacgtac gcgtgcatgc 327

tagctcatag ctcttctata gtgtcaccta aattcaattc actggccgtc gttttacaac 387

gtcgtgactg ggaaaaccct ggcgttaccc aacttaatcg ccttgcagca catccccctt 447

tcgccagctg gcgtaataag cgaagaggcc cgcaccgatc gcccttccca acagttgcgc 507

agcctgaatg gcgaaatggg acgcgccctg 537

<210> 240
<211> 34
<212> PRT
<213> Conus marmoreus

<400> 240
Glu Lys Arg Ala Cys Ser Lys Lys Trp Glu Tyr Cys Ile Val Pro Ile
1 5 10 15

Leu Gly Phe Val Tyr Cys Cys Pro Gly Leu Ile Cys Gly Pro Phe Val
20 25 30

Cys Val

<210> 241
<211> 31
<212> PRT

<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residue 6 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residues 8 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12, 21 and 27 may be Pro or hydroxy-Pro

<400> 241
Ala Cys Ser Lys Lys Xaa Xaa Xaa Cys Ile Val Xaa Ile Leu Gly Phe
1 5 10 15

Val Xaa Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Val
20 25 30

<210> 242
<211> 881
<212> DNA
<213> Conus omaria

<220>
<221> CDS
<222> (149)..(271)

<400> 242
aaagcaggta cgcctgcagg taccggtccg gaattcccgg gtcgacatca tcatcatcat 60

cgatccatct gtccattcat ccattcattc attcactgcc aaactgtcat aaatatttga 120

gtctttcttt ctgtttttat ctgacaga ttg aac gag aga gac tgc ctt aat 172
Leu Asn Glu Arg Asp Cys Leu Asn
1 5

gtt gat tat ttt tgt ggc ata ccg ttt gtg aac aac ggg cta tgc tgc 220
Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys Cys
10 15 20

agt ggc aat tgt gtt ttt tgt ctg cac acc cca agg gaa gta aaa ctg 268
Ser Gly Asn Cys Val Phe Cys Leu His Thr Pro Arg Glu Val Lys Leu
25 30 35 40

tca tgatgtcttc tcttcccctc tagtagtagt aggcggccgc tctagaggat 321
Pro

ccaaagcttac gtacgcgtgc atgcgacgtc atagctcttc tatagtgtca cctaaattca 381

attcactggc cgtcgtttta caacgtcgtg actgggaaaa ccctggcgtt acccaactta 441

atcgccttgc agcacatccc cctttcgcca gctggcgtaa tagcgaagag gcccgcaccg 501

atcgccctcc ccaacagttg cgcagcctga atggcgaatg ggacgcgccc t 552

<210> 243
<211> 41
<212> PRT
<213> Conus omaria

<400> 243
Leu Asn Glu Arg Asp Cys Leu Asn Val Asp Tyr Phe Cys Gly Ile Pro
1 5 10 15

Phe Val Asn Asn Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu
20 25 30

Xaa Thr Pro Arg Glu Val Lys Leu Pro
35 40

<210> 244
<211> 37
<212> PRT
<213> Conus omaria

<220>
<221> SITE
<222> (1)..(37)
<223> Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12, 31 and 37 m
ay be Pro or hydroxy-Pro; Xaa at residue 33 may be Glu or gamma-c
arboxy-Glu

<400> 244
Asp Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn
1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu His Thr Xaa Arg
20 25 30

Xaa Val Lys Leu Xaa
35

<210> 245
<211> 217
<212> DNA
<213> Conus obscurus

<220>
<221> CDS
<222> (36)..(181)

<400> 245
acatccatct gtccatccat ccattcattc attcattgcc aaactgtaac aaatattcaa 60

gtcctctctt ctgtttgtgt ctgac aga tcg aaa cgg tgc ctt gtt tac ggt 113
Arg Ser Lys Arg Cys Leu Val Tyr Gly
1 5

aca cct tgt gac tgg ctg acc att gcg ggt atg gag tgc tgc agt aaa 161
Thr Pro Cys Asp Trp Leu Thr Ile Ala Gly Met Glu Cys Cys Ser Lys
10 15 20 25

aag tgc ttt atg atg tgc tgg taaaactgcc gtgatgtctt ctactccccc c 212
Lys Cys Phe Met Met Cys Trp
30

<210> 246
<211> 37
<212> PRT
<213> Conus obscurus

<400> 246
Arg Ser Lys Arg Cys Leu Val Tyr Gly Thr Pro Cys Asp Trp Leu Thr
1 5 10 15

Ile Ala Gly Met Glu Cys Cys Ser Lys Lys Cys Phe Met Met Cys Trp
20 25 30

<10> 247
<11> 28
<12> PRT
<13> Conus obscurus

<220>
<221> SITE
<222> (1)..(28)
<223> Xaa at residue 4 may be Tyr, 125-I-Tyr, monc-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or
hydroxy-Pro; Xaa at residues 10 and 28 may be Trp or bromo-Trp; X
aa at residue 17 may be Glu or gamma-carboxy-Glu

<400> 247
Cys Leu Val Xaa Gly Thr Xaa Cys Asp Xaa Leu Thr Ile Ala Gly Met
1 5 10 15

Xaa Cys Cys Ser Lys Lys Cys Phe Met Met Cys Xaa
20 25

<10> 248
<11> 139
<12> DNA
<13> Conus radiatus

<220>
<221> CDS
<222> (1)..(108)

<400> 248
tgt aac cag aga gac tgc cat gaa gtt ggt gaa ttt tgt ggc tta ccg 49
Leu Asn Gln Arg Asp Cys His Glu Val Gly Glu Phe Cys Gly Leu Pro
1 5 10 15

tta ata aag aac ggg cta tgc tgc agt cag att tgt tta ggt gtc tgc 97
Leu Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys
20 25 30

gca aaa gtg ttt taaaactgcc gtgatgtctt ctactcccat 139
Ala Lys Val Phe
35

<10> 249
<11> 36
<12> PRT
<13> Conus radiatus

<400> 249
Leu Asn Gln Arg Asp Cys His Glu Val Gly Glu Phe Cys Gly Leu Pro
1 5 10 15

Leu Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys
20 25 30

Ala Lys Val Phe
35

<10> 250
<11> 36
<12> PRT
<13> Conus radiatus

<220>
<221> SITE

(1)..(42)
Xaa at residues 4 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 12 may be Pro or hydroxy-Pro

Asp Cys His Xaa Val Gly Xaa Phe Cys Gly Leu Xaa Leu Ile Lys Asn
1 5 10 15

Gly Leu Lys Cys Ser Gln Ile Cys Leu Gly Val Cys Ala Lys Val Phe
20 25 30

DNA
Conus radiatus

(1)..(100)

gac aag aaa gag tgc act gcc aat ggt gaa ttt tgt ggc ata tcg 49
Asp Lys Lys Glu Cys Thr Ala Asn Gly Glu Phe Cys Gly Ile Ser
1 5 10 15

ttt tga aac tac cta tgc tgc agt ggc cgg tgt gta ttc gtc tgc 97
Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys
20 25 30

tag tgaaact gccgtgatgt cttctacccc cat 133

PRT
Conus radiatus

Asp Lys Lys Glu Cys Thr Ala Asn Gly Glu Phe Cys Gly Ile Ser
1 5 10 15

Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys
20 25 30

Ile

PRT
Conus radiatus

SITE
(1)..(29)
Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r
esidue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
lpho-Tyr or O-phospho-Tyr

Xaa Cys Thr Ala Asn Gly Xaa Phe Cys Gly Ile Ser Val Phe Gly Ser
1 5 10 15

Xaa Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys Ile
20 25

<10> 254
<11> 1
<12> DNA
<13> Conus radiatus

<220>
<221> CDS
<222> (1)..(100)

<400> 254
a ttg gat aag aaa gag tgc act acc aat ggt gaa ttt tgt ggc ata tcg 49
Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser
1 5 10 15

gtg ttt gca agc ttc cta tgc tgc agt ggc ctg tgt gta ttc gtc tgc 97
Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys
20 25 30

atc tagctgaact gccgtgatgt cttctcttcc cct 133
Ile

<210> 255
<211> 33
<212> PRT
<213> Conus radiatus

<400> 255
Leu Asp Lys Lys Glu Cys Thr Thr Asn Gly Glu Phe Cys Gly Ile Ser
1 5 10 15

Val Phe Ala Ser Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys
20 25 30

Ile

<210> 256
<211> 33
<212> PRT
<213> Conus radiatus

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residues 1 and 7 may be Glu or gamma-carboxy-Glu.

<400> 256
Xaa Cys Thr Thr Asn Gly Xaa Phe Cys Gly Ile Ser Val Phe Ala Ser
1 5 10 15

Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys Ile
20 25

<210> 257
<211> 153
<212> DNA
<213> Conus radiatus

<220>
<221> CDS
<222> (1)..(100)

<400> 257
atg gat aag aga aaa tgc ttt ccc aaa aat cat ttt tgt ggc ttt gtg 49
Leu Asp Lys Arg Lys Cys Phe Pro Lys Asn His Phe Cys Gly Phe Val

1 5 10 15

grg atg ctg aac tac cta tgc tgc agt ggc cgg tgt ata ttc gtc tgc 97
Val Met Leu Asn Tyr Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys
20 25 30

gtc taattgaact gacgtgatgt cttctactcc cat 133
Val

<210> 256
<211> 33
<212> PRT
<213> Genus radiatus

<400> 256
Leu Asp Lys Arg Lys Cys Phe Pro Lys Asn His Phe Cys Gly Phe Val
1 5 10 15

Val Met Leu Asn Tyr Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys
20 25 30

Val

<210> 257
<211> 33
<212> PRT
<213> Genus radiatus

<220>
<221> SITE
<222> 1..(29)
<223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 257
Lys Cys Phe Xaa Lys Asn His Phe Cys Gly Phe Val Val Met Leu Asn
1 5 10 15

Xaa Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys Val
20 25

<210> 258
<211> 130
<212> DNA
<213> Genus regius

<220>
<221> CDS
<222> (1)..(99)

<400> 60
ttg aat aag aga agc tgc ctt cct cta gac tgg ttt tgt ggc ttc aat 48
Leu Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Asn
1 5 10 15

gta att gga gcg ttt ctg tgc tgt agt ggc tac tgc ctt gtc gtc tgc 96
Val Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys
20 25 30

gtt taaaactgac gtgatgtctt ctcctccct c 130
Val

<210> 261

<211> 32
<212> PRT
<213> Canus regius

<400> 101
Met Asn Lys Arg Ser Cys Leu Pro Leu Asp Trp Phe Cys Gly Phe Asn
1 5 10 15

Phe Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys
20 25 30

Met

<210> 102
<211> 33
<212> PRT
<213> Canus regius

<220>
<221> SITE
<222> (1)..(33)
<223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Trp or bromo-Trp; Xaa at residue 23 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 102
Met Lys Leu Xaa Leu Asp Xaa Phe Cys Gly Phe Asn Ile Ile Gly Ala
1 5 10 15

Phe Leu Cys Cys Ser Gly Xaa Cys Leu Val Val Cys Met
20 25

<210> 103
<211> 519
<212> DNA
<213> Canus dalessertii

<220>
<221> CDS
<222> (1)..(285)

<400> 103
atg aaa ctg acg tgt ctg ctg atc gtt gct gtg ctg gtc ttg gca gcc 48
Met Lys Leu Thr Cys Leu Leu Ile Val Ala Val Leu Val Leu Ala Ala
1 5 10 15

tgt cag ttc atc gta gct ggc gac tcg agt gat ggc cag gag aat cct 96
Cys Gln Phe Ile Val Ala Gly Asp Ser Ser Asp Gly Gln Glu Asn Pro
20 25 30

act ctg agg tca cct agc gat tcc tct ggg aaa atg tca tca atg aag 144
Thr Leu Arg Ser Pro Ser Asp Ser Ser Gly Lys Met Ser Ser Met Lys
35 40 45

ttc ttt cag tca cgg ctg atg gtg ggg caa tct gca tcg aaa aga cca 192
Arg Phe Gln Thr Arg Leu Met Val Gly Gln Ser Ala Ser Lys Arg Pro
50 55 60

agt aag agg gac tgc atc ccc ggc ggc gaa aat tgt gat gta ttc cga 240
Ser Lys Arg Asp Cys Ile Pro Gly Gly Glu Asn Cys Asp Val Phe Arg
65 70 75 80

tta tac cgg tgc tgc agt gga tat tgc ata cta ctc ctt tgc gca 285
Leu Tyr Arg Lys Cys Ser Gly Tyr Cys Ile Leu Leu Leu Cys Ala

85 90 95

tgataaagct gccttgatgt cttctcctcc ccta 319

<210> 204
<211> 97
<212> PRT
<213> Conus delessertii

<400> 204
Met Lys Leu Thr Cys Leu Leu Ile Val Ala Val Leu Val Leu Ala Ala
1 5 10 15

Cys Gln Phe Ile Val Ala Gly Asp Ser Ser Asp Gly Gln Glu Asn Pro
20 25 30

Ala Leu Arg Ser Pro Ser Asp Ser Ser Gly Lys Met Ser Ser Met Lys
35 40 45

Arg Phe Gln Thr Arg Leu Met Val Gly Gln Ser Ala Ser Lys Arg Pro
50 55 60

Ser Lys Arg Asp Cys Ile Pro Gly Gly Glu Asn Cys Asp Val Phe Arg
65 70 75 80

Ile Tyr Arg Cys Cys Ser Gly Tyr Cys Ile Leu Leu Leu Cys Ala
85 90 95

<210> 205
<211> 28
<212> PRT
<213> Conus delessertii

<220>
<221> SITE
<222> (1)..(28)
<223> Xaa at residues 4 and 14 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residues 15 and 21 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 205
Asp Cys Ile Xaa Gly Gly Xaa Asn Cys Asp Val Phe Arg Xaa Xaa Arg
1 5 10 15

Cys Cys Ser Gly Xaa Cys Ile Leu Leu Leu Cys Ala
20 25

<210> 206
<211> 1609
<212> DNA
<213> Conus striatus

<220>
<221> CDS
<222> (147)..(293)

<220>
<221> misc_feature
<222> (1)..(1009)
<223> n may be any nucleotide

<400> 206
gctggttagc ctgcaggtac cggtccggaa ttcccgggtc gacatcatca tcatcgatcc 60

atctgtccat ccatctattc attcattcat tcgctgccaa actgtattaa atattcaagt 100

ctct ttttct gtttgtgtct aacaga ttg aga tgg tgc att cct agt ggt gaa 138
Leu Arg Trp Cys Ile Pro Ser Gly Glu
1 5

ctt tgt ttc cgc tcg gat cac ata gga tgc tgt agt ggc aag tgc gca 231
Leu Cys Phe Arg Ser Asp His Ile Gly Cys Cys Ser Gly Lys Cys Ala
10 15 20 25

ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcttcccat ctagtagtag 278
Phe Val Cys Leu

tagctgccg ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt 338

ctctaatgtg acctaaattc aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa 398

accctggcgt tacccaactt aatcgccttg cagcacatcc cccttttcgcc agctggcgta 458

atagcgaaga ggcccgcacc gatcgcccct tcccaacagtt tgcgcagcct gaatggcgaa 518

tgggacgcgc cctgtagcgg cgcattaaac gcgggcgggt gtgggtgggt tacgcccacg 578

tgaccgcgcta cacttgccag cgccctancg cccgctccct ttcgctttct tcccttcct 638

tt ctcgncac gtttcggccg nttttcccg tcaagctctt aaatcgggggg gcttcccttt 698

aagggttncc gaattantgc tttacccggna ccttgacccc ccaaaaaaac ttggantaag 758

cgggcgatggn tcncgtaant ggggggccatc ncccctgaan agaacggttt ttcncccctt 818

ttgancngttg ggngttccnc ggttttttaaa aaanngggacc ttttnttttcc aaaactggga 878

ancancctaa accctatttt tggggctatt ttttgantt tnaaanggga ttttgcccca 938

ttttnggccc tnttggggta aaaaaaaqag ccggttttaa aaaaaatttt accccaaatt 998

ttaaaaaaaa tttttt 1014

<210> 167
<211> 29
<212> PRT
<213> Conus striatus

<400> 167
Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys Phe Arg Ser Asp His
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
20 25

<210> 168
<211> 29
<212> PRT
<213> Conus striatus

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residue3 may be Trp or bromo-Trp; Xaa at residue 6 may be Pro or hydroxy-Pro; Xaa at residue 9 may be Glu or gamma-carboxy-Glu

<...> 268
Leu Arg Xaa Cys Ile Xaa Ser Gly Xaa Leu Cys Phe Arg Ser Asp His
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
20 25

<...> 268
<...> 96
<...> DNA
<...> Conus striatus

<...>
<...> CDS
<...> (1)..(87)

<...> 268
Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
20 25

<...> 270
<...> 90
<...> DNA
<...> Conus striatus

<...> 270
Leu Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
20 25

<...> 271
<...> 27
<...> PRT
<...> Conus striatus

<...>
<...> SITE
<...> (1)..(27)
<...> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be Pro or hydroxy-Pro

<...> 271
Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Arg Ser Asp His Ile Gly
1 5 10 15

Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
20 25

<...> 272
<...> 90
<...> DNA
<...> Conus striatus

<...>
<...> CDS
<...> (1)..(87)

<400> 272
tcg aga tgg tgc att cct agt ggt gat ctt tgt ttc cgc tcg gat cac 48
Ser Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His
1 5 10 15

cta caa tgc tgc agt ggc aag tgc gca ttc gtc tgc ttg taa 90
Leu Gln Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
20 25

<210> 273
<211> 29
<212> PRT
<213> Conus striatus

<400> 273
Ser Arg Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Arg Ser Asp His
1 5 10 15

Leu Gln Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
20 25

<210> 274
<211> 27
<212> PRT
<213> Conus striatus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue1 may be Trp or bromo-Trp; Xaa at residue 4 may be Pro or hydroxy-Pro

<400> 274
Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Arg Ser Asp His Ile Gln
1 5 10 15

Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
20 25

<210> 275
<211> 206
<212> DNA
<213> Conus obscurus

<220>
<221> CDS
<222> (77)..(175)

<400> 275
gaatccattt gtccatccat ccattcagtc attcgctgcc aaactgtaac aaatattcaa 60

gtcaatgctt ctagttt gtg tct gac aga ctg aga tgg tgc gtt cct agc ggt 112
Val Ser Asp Arg Leu Arg Trp Cys Val Pro Ser Gly
1 5 10

aaa gtt tgt tgc cgc tat gaa ttc gtg gga tgc tgc agt ggc aag tgc 160
Lys Val Cys Arg Arg Tyr Glu Phe Val Gly Cys Cys Ser Gly Lys Cys
15 20 25

ttc ttc gtc tgc tag taaaactgtt gtgatgtctt ctcctccact c 206
Phe Phe Val Cys Ser
30

<210> 276

<211> 33
<212> PRT
<213> Conus obscurus

<400> 276
Val Ser Asp Arg Leu Arg Trp Cys Val Pro Ser Gly Glu Val Cys Arg
1 5 10 15

Arg Tyr Glu Phe Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys
20 25 30

Ser

<210> 277
<211> 29
<212> PRT
<213> Conus obscurus

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residue 3 may be Trp or bromo-Trp; Xaa at residue 6 may be Pro or hydroxy-Pro; Xaa at residues 9 and 15 may be Glu or gamma-carboxy-Glu; Xaa at residue 14 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 277
Leu Arg Xaa Cys Val Xaa Ser Gly Xaa Val Cys Arg Arg Xaa Xaa Phe
1 5 10 15

Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys Ser
20 25

<210> 278
<211> 159
<212> DNA
<213> Conus radiatus

<220>
<221> CDS
<222> (12)..(117)

<400> 278
atgtctctat ctctgctgga c agg tcg act cgc tgc ttg cct gac gga acg 51
Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr
1 5 10

tct tgc ctt ttt agt agg atc aga tgc tgc ggt act tgc agt tca atc 99
Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile
15 20 25

tta aag tca tgt gtg agc tgatccggcg gttgatcttc ctccctctgt 147
Leu Lys Ser Cys Val Ser
30

gtccatttct tttctgcctg agtcctcctt acctgagagt ggtcatgaac cactcatcac 207

ctgatcctct ggaggcttca gaggagctac attgaaataa aagccgcatt gc 259

<210> 279
<211> 33
<212> PRT
<213> Conus radiatus

<400> 279
Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg
1 5 10 15

Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25 30

<210> 280
<211> 29
<212> PRT
<213> Conus radiatus

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residue 3 may be Pro or hydroxy-Pro.

<400> 280
Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1 5 10 15

Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25

<210> 281
<211> 478
<212> DNA
<213> Conus geographus

<220>
<221> CDS
<222> (38)..(513)

<400> 281
gaatcttgca cggtgaattt cgcttcatat ttttctactg tcgtctttgg catcatccaa 60

aacatcacca ag atg aaa ctg acg tgc atg atg att gtt gct gtg ctg ttc 111
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe
1 5 10

ttg acc gcc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta 159
Leu Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val
15 20 25

ttg gag aat ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa 207
Leu Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu
30 35 40 45

gcc tct aaa ttg aac gtg aga gac gac gag tgc gaa cct cct gga gat 255
Ala Ser Lys Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp
50 55 60

ttt tgt ggc ttt ttt aaa att ggg ccg cct tgc tgc agt ggc tgg tgc 303
Phe Cys Gly Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys
65 70 75

att ctc tgg tgc gcc taaaactgcc gtgatgtctt ctattcccct ctgtgctacc 358
Ile Leu Trp Cys Ala
80

tggcttgatc tttgattggc gcgtgccctt cagtggttat gaaccccccc gagccgactc 418

tctgggggtc tcgggggttc aacatccaaa taaagcgaca acacaatcac aagtaaaaaa 478

<200> 282
<211> 82
<212> PRT
<213> Conus geographus

<400> 282
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val Leu Glu Asn
20 25 30

Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu Ala Ser Lys
35 40 45

Leu Asn Val Arg Asp Asp Glu Cys Glu Pro Pro Gly Asp Phe Cys Gly
50 55 60

Phe Phe Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Leu Trp
65 70 75 80

Cys Ala

<210> 283
<211> 30
<212> PRT
<213> Conus geographus

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residues 3and 5 may be Glu or gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues 24 and 28 may be Trp or bromo-Trp

<400> 283
Asp Asp Xaa Cys Xaa Xaa Xaa Gly Asp Phe Cys Gly Phe Phe Lys Ile
1 5 10 15

Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Leu Xaa Cys Ala
20 25 30

<210> 284
<211> 318
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (3)..(164)

<220>
<221> misc_feature
<222> (1)..(318)
<223> n may be any nucleotide

<400> 284
gc tgc agg tcg act cta gag gcg ttg gag aat ctt tat ctg aag gca 47
Cys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala
1 5 10 15

cat cat gaa atg aac aac ccc gaa gac tct gaa ttg aac aag agg tgc 95
His His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys
20 25 30

```
tat gat agt ggg aca agt tgt aac act gga aac caa tgc tgc agt ggc      143
Tyr Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly
            35                  40                  45

tgg tgc att ttc gtc tgc ctc taaaactgcc gtgatgtctt ctactcccct      194
Trp Cys Ile Phe Val Cys Leu
        50

ctgtgctacc tacctggctt gatctttgat tggcggtgtc ccttcactgg ttatgaaccc  254

ctctcatccg actctctggg ggcctcgggg atccaacatc aaaatanagc gacagcacaa  314

tgac                                                              318

<210>  185
<211>  54
<212>  PRT
<213>  Conus textile

<400>  185
Cys Arg Ser Thr Leu Glu Ala Leu Glu Asn Leu Tyr Leu Lys Ala His
1               5                  10                  15

His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys Tyr
            20                  25                  30

Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp
        35                  40                  45

Cys Ile Phe Val Cys Leu
    50

<210>  186
<211>  54
<212>  PRT
<213>  Conus textile

<220>
<221>  SITE
<222>  (2)..(24)
<223>  Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
       r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
       bromo-Trp

<400>  186
Cys Xaa Asp Ser Gly Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser
1               5                  10                  15

Gly Xaa Cys Ile Phe Val Cys Leu
            20

<210>  187
<211>  480
<212>  DNA
<213>  Conus quercinus

<220>
<221>  CDS
<222>  (52)..(333)

<400>  187
gcttcgtatt tctccgctgt cttccttggc atcacccaaa acatcaccaa g atg aaa      57
                                                        Met Lys
                                                        1
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```
ctg acg tgc atg atg atc gtt gct ctg ctg ttc ttg acc gcc tgg aca      105
Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala Trp Thr
 1               5                  10                  15

ttc gtc acg gct gtt gac tcc aaa aat gaa ctg gag aac aga gga gga      153
Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg Gly Gly
            20                  25                  30

tgg ggg cag gca gga gga tgg ggg aaa ctt ttt ccg atg gca cgc gac      201
Trp Gly Gln Ala Gly Gly Trp Gly Lys Leu Phe Pro Met Ala Arg Asp
        35                  40                  45                  50

gaa atg aaa aac agc gaa gtc tct aaa ttg gac aat aag aga aag tgc      249
Glu Met Lys Asn Ser Glu Val Ser Lys Leu Asp Asn Lys Arg Lys Cys
                    55                  60                  65

gct gca gcc ggt gaa gct tgc gta ata cct atc att gga aac gta ttt      297
Ala Ala Ala Gly Glu Ala Cys Val Ile Pro Ile Ile Gly Asn Val Phe
                70                  75                  80

tgc tgc aaa ggc tac tgt ctt ttc gtc tgc att agt taaactgctg           343
Cys Cys Lys Gly Tyr Cys Leu Phe Val Cys Ile Ser
            85                  90

tnatgccttc tactcaccta tgtgctacct ggcttgatct ttgattggca tgtgcccttc    403

acttgattta tt agctccgtctg atcctactct ctggagacct ctgtggtcca acatccaaat  463

aaaacaggcat cccaatg                                                  480

<210>  188
<211>  94
<212>  PRT
<213>  Conus quercinus

<400>  188
Met Lys Leu Thr Cys Met Met Ile Val Ala Leu Leu Phe Leu Thr Ala
 1               5                  10                  15

Trp Thr Phe Val Thr Ala Val Asp Ser Lys Asn Glu Leu Glu Asn Arg
            20                  25                  30

Gly Gly Trp Gly Gln Ala Gly Gly Trp Gly Lys Leu Phe Pro Met Ala
        35                  40                  45

Arg Asp Glu Met Lys Asn Ser Glu Val Ser Lys Leu Asp Asn Lys Arg
    50                  55                  60

Lys Cys Ala Ala Ala Gly Glu Ala Cys Val Ile Pro Ile Ile Gly Asn
65                  70                  75                  80

Val Phe Cys Cys Lys Gly Tyr Cys Leu Phe Val Cys Ile Ser
                85                  90

<210>  189
<211>  94
<212>  PRT
<213>  Conus quercinus

<220>
<221>  SITE
<222>  (1)..(29)
<223>  Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
       11 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Tyr, 125-I
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-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 290
Cys Ala Ala Ala Gly Xaa Ala Cys Val Ile Xaa Ile Ile Gly Asn Val
1 5 10 15

Xaa Cys Cys Lys Gly Xaa Cys Leu Phe Val Cys Ile Ser
20 25

<210> 291
<211> 410
<212> DNA
<213> Conus leopardus

<220>
<221> CDS
<222> (1)..(246)

<400> 291
atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

acg ata ttc atc acg act gat gac tcc aca aat gga ctg gag aat cgt 96
Thr Ile Phe Ile Thr Ala Asp Asp Ser Thr Asn Gly Leu Glu Asn Arg
20 25 30

ttt agg aag gca cgt gac aac atg aag aac gcc aaa gcc tct aca tta 144
Phe Arg Lys Ala Arg Asp Asn Met Lys Asn Ala Lys Ala Ser Thr Leu
35 40 45

gca gag aag aaa gcg tgt gtt gaa ctt ggt gag att tgt gcc aca ggc 192
Ala Glu Lys Lys Ala Cys Val Glu Leu Gly Glu Ile Cys Ala Thr Gly
50 55 60

tgc ttc cta gac gag gaa tgc tgc act ggt tca tgc cat gtc ttc tgc 240
Cys Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys
65 70 75 80

tga cta tagttaaact gctgtgatgt cttcttctct cctcagtgct acctggcttg 296
Val Leu

atttttgatt ggtgcctgtc cttcagtggt tgtgaaaccc tctgatccta ctctctggac 356

gcttctgagg cccaacatcc aaataaagcg acatcctaat gtcaaaaaaa aaaa 410

<210> 291
<211> 80
<212> PRT
<213> Conus leopardus

<400> 291
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Thr Ile Phe Ile Thr Ala Asp Asp Ser Thr Asn Gly Leu Glu Asn Arg
20 25 30

Phe Arg Lys Ala Arg Asp Asn Met Lys Asn Ala Lys Ala Ser Thr Leu
35 40 45

Ala Glu Lys Lys Ala Cys Val Glu Leu Gly Glu Ile Cys Ala Thr Gly
50 55 60

Phe Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys
65 70 75 80

Val Leu

<211> 242
<212> PRT
<213> Conus leopardus

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residues 4, 7, 17 and 18 may be Glu or gamma-carboxy-Glu.

<400> 242

Ala Cys Val Xaa Leu Gly Xaa Ile Cys Ala Thr Gly Phe Phe Leu Asp
1 5 10 15

Xaa Xaa Cys Cys Thr Gly Ser Cys His Val Phe Cys Val Leu
20 25 30

<210> 243
<211> 336
<212> DNA
<213> Conus marmoreus

<220>
<221> CDS
<222> (1)..(231)

<400> 243

atg aaa ctg acg tac gtg gtg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

ttg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gag aat ctt 96
Leu Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

ttt tcg aag gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aat aag agg tgc cct aac act ggt gaa tta tgt gat gtg gtt gaa caa 192
Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
50 55 60

aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta taaaactacc 241
Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
65 70 75

ttgatgtctt ctactccact ctgtgctgcc tggcttgatc tttgattggc gcgtgcccct 301

tatttgttat gacccccctg atccgacctc tgggg 336

<210> 244
<211> 77
<212> PRT
<213> Conus marmoreus

<400> 244

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala

1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Pro Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
50 55 60

Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
65 70 75

<210> 295
<211> 26
<212> PRT
<213> Conus marmoreus

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 3 may be Pro or hydroxy-Pro; Xaa at residues 6 and 11 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 295
Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu
20 25

<210> 296
<211> 480
<212> DNA
<213> Conus quercinus

<220>
<221> CDS
<222> (3)..(240)

<400> 296
gg atg aaa ctg acg tgt atg gtg atc gtt gct gtg cta ttc ttg 48
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tcg gct gat gac tcc aga aat gga ttc gag aat cga aat gga 96
Thr Ala Ser Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly
15 20 25 30

gaa cga aac gaa aac gaa atg aag aac ctc gaa gcc tct aaa ttg aac 144
Glu Arg Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn
35 40 45

aac aga gac ggc gat tgc gtt gat ggt ggt gaa ttt tgt ggc ttt ccg 192
Asn Arg Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro
50 55 60

aaa att gga ggg cca tgc tgt agt ggc tgg tgc ttt ttc gtc tgc tta 240
Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
65 70 75

taaactgtc atgatgtctt ctacccccct ctgtgctacc tgacttgatc tttgattggc 300

gtgtccctt cactggttat gaaccgctct gatccgactc tctggaggcc tcgggggtcc 360

aaaaaaaaaa taaagcgaca gcaaaaaaaa aaaaaaaaaa aa 402

<210> 297
<211> 78
<212> PRT
<213> Conus quercinus

<400> 297
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Val Ala Asp Asp Ser Arg Asn Gly Phe Glu Asn Arg Asn Gly Glu Arg
20 25 30

Asn Glu Asn Glu Met Lys Asn Leu Glu Ala Ser Lys Leu Asn Arg Arg
35 40 45

Asp Gly Asp Cys Val Asp Gly Gly Glu Phe Cys Gly Phe Pro Lys Ile
50 55 60

Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
65 70 75

<210> 298
<211> 30
<212> PRT
<213> Conus quercinus

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residue 9 may be Glu or gamma-carboxy-Glu; Xaa at residues 14 and 19may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp

<400> 298
Asp Gly Asp Cys Val Asp Gly Gly Xaa Phe Cys Gly Phe Xaa Lys Ile
1 5 10 15

Gly Gly Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu
20 25 30

<210> 299
<211> 274
<212> DNA
<213> Conus quercinus

<220>
<221> CDS
<222> (7)..(216)

<220>
<221> misc_feature
<222> (1)..(274)
<223> n may be any nucleotide

<400> 299
ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg cta ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

```
acc gcc ttg gct gat gac tcc aga aat gga ttg gag aat cga aat gaa          96
Thr Ala Leu Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Arg Asn Glu
1               5                  10                  15

caa gaa aga aac gaa aac gaa atg agg gac cgc cgg gac tgc caa gat          144
Gln Glu Arg Asn Glu Asn Glu Met Arg Asp Arg Arg Asp Cys Gln Asp
            20                  25                  30

agt ggt gta gtt tgt ggc ttt ccg aaa cct gaa cca cac tgc tgc agt          192
Ser Gly Val Val Cys Gly Phe Pro Lys Pro Glu Pro His Cys Cys Ser
        35                  40                  45

ggt tgg tgc ctt ttc gtc tgc gcc taaaactgcc gtgatgtcaa ataaagcgac        246
Gly Trp Cys Leu Phe Val Cys Ala
    50                  55

agtcaatnaa aaaaaaaaaa aaaaaaaa                                          274

<210> 309
<211> 70
<212> PRT
<213> Conus quercinus

<400> 309
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

Leu Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Arg Asn Glu Gln Glu
            20                  25                  30

Arg Asn Glu Asn Glu Met Arg Asp Arg Arg Asp Cys Gln Asp Ser Gly
        35                  40                  45

Val Val Cys Gly Phe Pro Lys Pro Glu Pro His Cys Cys Ser Gly Trp
    50                  55                  60

Cys Leu Phe Val Cys Ala
65                  70

<210> 301
<211> 28
<212> PRT
<213> Conus quercinus

<220>
<221> SITE
<222> (1)..(28)
<223> Xaa at residues 12, 14 and 16 may be Pro or hydroxy-Pro; Xaa at r
      esidue15 may be Glu or gamma-carboxy-Glu; Xaa at residue 22 may b
      e Trp or bromo-Trp

<400> 301
Asp Cys Gln Asp Ser Gly Val Val Cys Gly Phe Xaa Lys Xaa Xaa Xaa
1               5                  10                  15

His Cys Cys Ser Gly Xaa Cys Leu Phe Val Cys Ala
            20                  25

<210> 302
<211> 340
<212> DNA
<213> Conus arenatus

<220>
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<221> CDS
<222> (7)..(246)

<220>
<221> misc_feature
<222> (1)..(340)
<223> n may be any nucleotide

<400> 302
gnatnc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

ang gcc tgg aca ttc gtc acg gct gac tcc ata cgt gca ctg gag gat 96
Thr Ala Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp
15 20 25 30

ttc ttt gcg aag gca cgt gac gaa atg gaa aac agc gga gct tct cca 144
Phe Phe Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro
35 40 45

ttg aac gag aga gac tgc cga cct gta ggt caa tat tgt ggc ata ccg 192
Leu Asn Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro
50 55 60

tac aag cac aac tgg cga tgc tgc agt cag ctt tgt gca att atc tgt 240
Tyr Lys His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys
65 70 75

gtt tnc taacccctct gatcctactc tctgaagacc tccgggattc aacatccaaa 296
Val Xaa
80

tnaaangaca tcccgatnaa aaaaaangaa aaaaaaaaaa aaaa 340

<210> 303
<211> 80
<212> PRT
<213> Conus arenatus

<400> 303
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp Phe Phe
20 25 30

Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro Leu Asn
35 40 45

Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro Tyr Lys
50 55 60

His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
65 70 75 80

<210> 304
<211> 30
<212> PRT
<213> Conus arenatus

<220>
<221> SITE
<222> (1)..(30)

<223> Xaa at residues 4 and 12 may be Pro or hydroxy-Pro; Xaa at residues 8 and 13 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 17 may be Trp or brom-Trp

<400> 304
Asp Cys Arg Xaa Val Gly Gln Xaa Cys Gly Ile Xaa Xaa Lys His Asn
1 5 10 15

Xaa Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
20 25 30

<210> 305
<211> 381
<212> DNA
<213> Conus arenatus

<220>
<221> CDS
<222> (7)..(334)

<400> 305
ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gtt gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttc gtc aag gct gat gac tcc ata aat gga ttg gag 96
Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu
15 20 25 30

aat ctt ttt ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ttg aac gag agg tgc ctt gaa aag ggt gta ctt tgt gat ccg agt 192
Lys Leu Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser
50 55 60

gct gga aac tgc tgt agt ggc gaa tgc gtt tta gtc tgc ctc 234
Ala Gly Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu
65 70 75

taaaactacc gtgatgtctt ctactcccat ctgtgctacc cctcgag 281

<210> 306
<211> 76
<212> PRT
<213> Conus arenatus

<400> 306
Met Lys Leu Thr Cys Val Val Ile Val Val Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser Ala Gly
50 55 60

Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu
65 70 75

<210> 307
<211> 25
<212> PRT
<213> Conus arenatus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residues 3 and 19 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Pro or hydroxy-Pro

<400> 307
Cys Leu Xaa Lys Gly Val Leu Cys Asp Xaa Ser Ala Gly Asn Cys Cys
1 5 10 15

Cys Gly Xaa Cys Val Leu Val Cys Leu
20 25

<210> 308
<211> 287
<212> DNA
<213> Conus arenatus

<220>
<221> CDS
<222> (7)..(240)

<400> 308
ggatcc atg aaa ctg acg tgc atg gtg atc gtt act gtg ttg ttc ttg 48
Met Lys Leu Thr Cys Met Val Ile Val Thr Val Leu Phe Leu
1 5 10

act gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gaa ttg gag 96
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu
15 20 25 30

aat ctt ttt ctg aag gca tat cac gaa atg aac tcc gaa gcc tct aaa 144
Asn Leu Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys
35 40 45

ttg gac aag aaa gag tgc gtt gct ggt agt cac ttt tgt ggt ttt ccg 192
Leu Asp Lys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro
50 55 60

aaa att gga ggg cca tgc tgc agt ggc tgg tgc ttt ttc gtc tgc ttg 240
Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
65 70 75

taaacctgcc gtgatgtctt ctactcccat ctgtgctacc cctcgag 287

<210> 309
<211> 78
<212> PRT
<213> Conus arenatus

<400> 309
Met Lys Leu Thr Cys Met Val Ile Val Thr Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu Asn Leu
20 25 30

Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys Leu Asp
35 40 45

Lys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro Lys Ile
50 55 60

Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
65 70 75

<210> 310
<211> 28
<212> PRT
<213> Conus arenatus

<220>
<221> SITE
<222> (1)..(28)
<223> Xaa at residue 1 may be Glu or gamma-carboxy-Glu; Xaa at residues 11 and 17 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Trp or bromo-Trp

<400> 310
Xaa Cys Val Ala Gly Ser His Phe Cys Gly Phe Xaa Lys Ile Gly Gly
1 5 10 15

Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu
20 25

<210> 311
<211> 400
<212> DNA
<213> Conus tessulatus

<220>
<221> CDS
<222> (71)..(243)

<400> 311
gcatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg atg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu
1 5 10

acc gcc tgg aca ttc atc acg gct gat gac tcc ata aat gga ctg gag 96
Thr Ala Trp Thr Phe Ile Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu
15 20 25 30

gat aga ggc ata tgg ggg gaa cct ttg tcg aag gca cgt gac gaa atg 144
Asp Arg Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met
35 40 45

aac ccc gaa gtc tct aaa cgg gat tgc tgg cct caa tat tgg ttt tgt 192
Asn Pro Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys
50 55 60

tgc cta cag agg gga tgc tgc cca ggg act act tgc ttc ttc ctt tgc 240
Gly Leu Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys
65 70 75

tga tgatctc ttcgactccc ttctgtgcta cctggcttga cctttgattg 293
Xaa

atgcctgccc ttcactggtt ataaaccccc ctgttcctcc tctctggacg cttcggggtg 353

aaaagcatcc aaataaaggg acgtccccaa aaaaaaaaaa aaaaaaa 400

<210> 312

<211> 79
<212> PRT
<213> Conus tessulatus

<400> 312
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Met Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ile Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asp Arg
20 25 30

Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met Asn Pro
35 40 45

Gln Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys Gly Leu
50 55 60

Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys Phe
65 70 75

<210> 313
<211> 26
<212> PRT
<213> Conus tessulatus

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3 and 7 may be Trp or bromo-Trp; Xaa at residues 4 and 17 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 313
Asp Cys Xaa Xaa Gln Xaa Xaa Phe Cys Gly Leu Gln Arg Gly Cys Cys
1 5 10 15

Xaa Gly Thr Thr Cys Phe Phe Leu Cys Phe
20 25

<210> 314
<211> 419
<212> DNA
<213> Conus tessulatus

<220>
<221> CDS
<222> (7)..(249)

<400> 314
gaattc atg aaa ctg acg tgc gtg gtg gtc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Val Val Ala Val Leu Phe Leu
1 5 10

aac gcc tgg aca ttc gcc acg gct gtt gac tcc aaa cat gca ctg gcg 96
Asn Ala Trp Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala
15 20 25 30

aaa ctt ttt atg aag gca cgt gac gaa atg tat aac ccc gat gcc act 144
Lys Leu Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr
35 40 45

aaa ttg gac gat aag aga tgg tgc gct tta gat ggt gaa ctt tgt atc 192
Lys Leu Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile

50 55 60

ata cag gtc att ggg tcc ata ttt tgc tgc cat ggc ata tgt atg atc 240
Ile Gln Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile
65 70 75

tac tgc gtc tagttgaact gccgtgatgt cttctactcc cctctgtgct 289
Tyr Cys Val
80

acccctggtt tgatctttga ttgccctgtg ccctttcactg attatgaatc cctctgatcc 349

tagtctctga agacctcttg gggtccaaca tccaaataaa gcgacatccc aaaaaaaaaa 409

aaaaaaaaaa 419

<210> 315
<211> 81
<212> PRT
<213> Conus tessulatus

<400> 315
Met Lys Leu Thr Cys Val Val Val Val Ala Val Leu Phe Leu Asn Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala Lys Leu
20 25 30

Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr Lys Leu
35 40 45

Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile Ile Pro
50 55 60

Val Ile Gly Ser Ile Phe Cys Cys His Gly Ile Cys Met Ile Tyr Cys
65 70 75 80

Val

<210> 316
<211> 29
<212> PRT
<213> Conus tessulatus

<220>
<221> SITE
<222> (1)..(29)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may b
e Glu or gamma-carboxy-Glu; Xaa at residue 12 may be Pro or hydro
xy-Pro; Xaa at residue 27 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, d
i-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 316
Xaa Cys Ala Leu Asp Gly Xaa Leu Cys Ile Ile Xaa Val Ile Gly Ser
1 5 10 15

Ile Phe Cys Cys His Gly Ile Cys Met Ile Xaa Cys Val
20 25

<210> 317
<211> 408
<212> DNA
<213> Conus imperialis

<220>
<221> CDS
<222> (7)..(240)

<400> 317
gaattcc atg aaa ctg acg tgc gtg gtg ttc gtt gct gtg ccg ttc ttg 48
Met Lys Leu Thr Cys Val Val Phe Val Ala Val Pro Phe Leu
1 5 10

acc gcc tcg gta ttc atc acg gct gat gac tcc aga aat gga atc gag 96
Thr Ala Ser Val Phe Ile Thr Ala Asp Asp Ser Arg Asn Gly Ile Glu
15 20 25 30

aat ctt cct cgg atg aga cgt cac gaa atg aag aac ccc aaa gcc tct 144
Asn Leu Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser
35 40 45

aag ttg aac aag aga cag tgc cgt gta gaa ggt gaa att tgt ggc atg 192
Lys Leu Asn Lys Arg Gln Cys Arg Val Glu Gly Glu Ile Cys Gly Met
50 55 60

ctg ttt gaa gca caa tgc tgc gat ggc tgg tgc ttt ttc gtc tgc atg 240
Leu Phe Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met
65 70 75

taaaactgcc gtgatgtctt ctactctcct ctgtgctacc tgccctgatc tttgattggc 300

tgtggcccct cattggttat gaacccctct gatcctactc tctggaggcc tcaggggtcc 360

agcaatctaaa taaagcgaca tcacaatcaa aaaaaaaaaa aaaaaaaa 408

<210> 318
<211> 79
<212> PRT
<213> Conus imperialis

<400> 318
Met Lys Leu Thr Cys Val Val Phe Val Ala Val Pro Phe Leu Thr Ala
1 5 10 15

Ser Val Phe Ile Thr Ala Asp Asp Ser Arg Asn Gly Ile Glu Asn Leu
20 25 30

Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
35 40 45

Asn Lys Arg Gln Cys Arg Val Glu Gly Glu Ile Cys Gly Met Leu Phe
50 55 60

Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met
65 70 75

<210> 319
<211> 27
<212> PRT
<213> Conus imperialis

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Gln or pyro-Glu; Xaa at residues 5, 7 and 14 may be Glu or gamma-carboxy-Glu; Xaa at residue 21 may be Trp or bromo-Trp

<400> 313
Xaa Cys Arg Val Xaa Gly Xaa Ile Cys Gly Met Leu Phe Xaa Ala Gln
1 5 10 15

Cys Cys Asp Gly Xaa Cys Phe Phe Val Cys Met
20 25

<210> 320
<211> 291
<212> DNA
<213> Conus caracteristicus

<220>
<221> CDS
<222> (7)..(234)

<400> 320
ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag 96
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu
15 20 25 30

aac ctt ttt ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct 144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ctg aac aag agg tgc gtt gac cct ggt gaa ttt tgt ggt ccg gga 192
Lys Leu Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly
50 55 60

ttt gga gat tgc tgc act ggc ttc tgc ctt tta gtc tgc atc 234
Phe Gly Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
65 70 75

taaaaactgcc gtgatgtctt ctactcccat ctgtgctacc cctcgag 281

<210> 321
<211> 76
<212> PRT
<213> Conus caracteristicus

<400> 321
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly Phe Gly
50 55 60

Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
65 70 75

<210> 322
<211> 35
<212> PRT
<213> Conus caracteristicus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residues 4 and 10 may be Pro or hydroxy-Pro; Xaa at residu
e 6 may be Glu or gamma-carboxy-Glu

<400> 323
Cys Val Asp Xaa Gly Xaa Phe Cys Gly Xaa Gly Phe Gly Asp Cys Cys
1 5 10 15

Thr Gly Phe Cys Leu Leu Val Cys Ile
20 25

<210> 323
<211> 297
<212> DNA
<213> Conus miliaris

<220>
<221> CDS
<222> (7)..(240)

<400> 323
gaatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ttg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc gct tgg aca ttc gtc atg gct gat gac tcc aga aat gat ttg gag 96
Thr Ala Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu
15 20 25 30

aat ctt ttt ctg aag gca cgt cat gaa atg aag aac ccc gaa gct tct 144
Asn Leu Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
35 40 45

aaa ttg aac aag aga tgc ctt cca aat ggt gta ctt tgt gat ctg gga 192
Lys Leu Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly
50 55 60

tct cca cca tac tgc tgc agt ggc tgg tgc gcg atc gtc gtc tgc atc 240
Ser Pro Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile
65 70 75

taaaactgtc gtcatgtctt ctactccat ctgtgctacc cctcgag 287

<210> 324
<211> 78
<212> PRT
<213> Conus miliaris

<400> 324
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu Asn Leu
20 25 30

Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly Ser Pro
50 55 60

Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile

65 70 75

<400> 325
<211> 27
<212> PRT
<213> Conus miliaris

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residues 3, 13 and 14 may be Pro or hydroxy-Pro; Xaa at residue 15 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 20 may be Trp or bromo-Trp

<400> 325
Cys Leu Xaa Asn Gly Val Leu Cys Asp Leu Gly Ser Xaa Xaa Xaa Cys
1 5 10 15

Cys Ser Gly Xaa Cys Ala Ile Val Val Cys Ile
20 25

<210> 326
<211> 247
<212> DNA
<213> Conus atlanticus

<220>
<221> CDS
<222> (7)..(240)

<400> 326
agatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttc gtc acg gct gat gac tcc ata aat ggg ttg gag 96
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu
15 20 25 30

aat ctt ttt ccg aag gca cgt cac gaa atg agg aaa ccc gaa gcc tct 144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Arg Lys Pro Glu Ala Ser
35 40 45

aga tcg aga ggg agg tgc cgt cct cgt ggt atg ttc tgt ggc ttt ccg 192
Arg Ser Arg Gly Arg Cys Arg Pro Arg Gly Met Phe Cys Gly Phe Pro
50 55 60

aaa cct gga cca tac tgc tgc aat ggc tgg tgc ttt ttc gtc tgc atc 240
Lys Pro Gly Pro Tyr Cys Cys Asn Gly Trp Cys Phe Phe Val Cys Ile
65 70 75

taaaactgcc gtgatgtgtt ctactcccat ctgtgctacc cctcgag 287

<210> 327
<211> 78
<212> PRT
<213> Conus atlanticus

<400> 327
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu

```
                20                  25                  30

Phe Pro Lys Ala Arg His Glu Met Arg Lys Pro Glu Ala Ser Arg Ser
        35                  40                  45

Asn Gly Arg Cys Arg Pro Arg Gly Met Phe Cys Gly Phe Pro Lys Pro
    50                  55                  60

Gly Pro Tyr Cys Cys Asn Gly Trp Cys Phe Phe Val Cys Ile
65                  70                  75

<210>  328
<211>  27
<212>  PRT
<213>  Conus atlanticus

<220>
<221>  SITE
<222>  (1)..(27)
<223>  Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa a
       t residue16  may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or bro
       mo-Trp

<400>  328
Cys Arg Xaa Arg Gly Met Phe Cys Gly Phe Xaa Lys Xaa Gly Xaa Xaa
1               5                  10                  15

Cys Cys Asn Gly Xaa Cys Phe Phe Val Cys Ile
            20                  25

<210>  329
<211>  264
<212>  DNA
<213>  Conus lividus

<220>
<221>  CDS
<222>  (7)..(267)

<400>  329
ggatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg          48
       Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
       1               5                  10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gag          96
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu
            20                  25                  30

aat ctt ttt tcg aag gca cat cac gaa atg aag aac ccc gaa gcc tct         144
Asn Leu Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser
        35                  40                  45

aaa ttg aac aag agg tgc cct aac act ggt gaa tta tgt gat gtg gtt         192
Lys Leu Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val
    50                  55                  60

cat caa aac tgc tgc tat acc tat tgc ttt att gta gtc tgc cta             237
His Gln Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
65                  70                  75

taaaactacc gtgatgtctt ctactcccat ctgtgctacc cctcgag                    284

<210>  330
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<211> 77
<212> PRT
<213> Conus lividus

<400> 330
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
20 25 30

Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Cys Pro Asn Thr Gly Glu Leu Cys Asp Val Val Glu Gln
50 55 60

Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
65 70 75

<210> 331
<211> 26
<212> PRT
<213> Conus lividus

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residue 2 may be Pro or hydroxy-Pro; Xaa at residues 6 and 11 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 331
Cys Xaa Asn Thr Gly Xaa Leu Cys Asp Val Val Xaa Gln Asn Cys Cys
1 5 10 15

Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu
20 25

<210> 332
<211> 291
<212> DNA
<213> Conus pulicarius

<220>
<221> CDS
<222> (7)..(234)

<400> 332
gaattc atg aaa ctg acg tgc atg gtg atc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu
1 5 10

act gcc tgg aca ttc gtc aag gct gat gac tcc aga aat gga ttg gag 96
Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu
15 20 25 30

aat ctt ttt ccg aag gca cgt cac gaa atg aag aac tcc aaa gcc tct 144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser
35 40 45

aaa tta aac aag agg tgc gtt gaa gat ggt gat ttt tgt ggt ccg gga 192
Lys Leu Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly

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            50                  55                  60

tat gaa gag tgc tgc agt ggc ttc tgc ctt tac gtc tgc atc                234
Tyr Glu Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile
        65                  70                  75

taaaactgcc gtgatgtctt ctactcccat ctgtgctacc cctcgag                    281

<210>  333
<211>  76
<212>  PRT
<213>  Conus pulicarius

<400>  333
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
            20                  25                  30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser Lys Leu
        35                  40                  45

Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly Tyr Glu
    50                  55                  60

Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile
65                  70                  75

<210>  334
<211>  25
<212>  PRT
<213>  Conus pulicarius

<220>
<221>  SITE
<222>  (1)..(25)
<223>  Xaa at residues 3, 13 and 14 may be Glu or gamma-carboxy-Glu; Xaa
       at residue 10 may be Pro or hydroxy-Pro; Xaa at residues 12 and
       22 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Ty
       r or O-phospho-Tyr

<400>  334
Cys Val Xaa Asp Gly Asp Phe Cys Gly Xaa Gly Xaa Xaa Xaa Cys Cys
1               5                  10                  15

Ser Gly Phe Cys Leu Xaa Val Cys Ile
            20                  25

<210>  335
<211>  249
<212>  DNA
<213>  Conus generalis

<220>
<221>  CDS
<222>  (1)..(249)

<400>  335
atg atc atg aaa ctg acg tgt gtg gtg ata gtt gct gtg cta ttc ttg          48
Met Ile Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1               5                  10

acc gcc tgg aca ttc gtc acg gct gat gac agc aga tat aaa ctg gag          96
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Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu
15 20 25 30

aat cct ttt ctg aag gca cgc aac gaa ctg cag aaa cac gaa gcc tct 144
Asn Pro Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser
35 40 45

caa ctg aac gag aga ggc tgc ctt gac cca ggt tac ttc tgt ggg acg 192
Gln Leu Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr
50 55 60

ccg ttt ctt gga gca tac tgc tgc ggt ggc att tgc ctt att gtc tgc 240
Pro Phe Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys
65 70 75

att gaa acg taaaggcttg atgtctttcta ctccgatctg tgctacccct cgag 293
Ile Glu Thr
80

<210> 336
<211> 81
<212> PRT
<213> Conus generalis

<400> 336
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu Asn Pro
20 25 30

Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser Gln Leu
35 40 45

Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr Pro Phe
50 55 60

Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Glu
65 70 75 80

Thr

<210> 337
<211> 30
<212> PRT
<213> Conus generalis

<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residues 5 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 337
Gly Cys Leu Asp Xaa Gly Xaa Phe Cys Gly Thr Xaa Phe Leu Gly Ala
1 5 10 15

Xaa Cys Cys Gly Gly Ile Cys Leu Ile Val Cys Ile Xaa Thr
20 25 30

<210> 338
<211> 400
<212> DNA

<213> Conus episcopatus

<220>
<221> CDS
<222> (7)..(234)

<400> 338
gtatcc atg aaa ctg acg tgc gtg gtg atc gtt gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg 96
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly
15 20 25 30

aat ctt ttt tcg aat gta cat cac gaa atg aag aac ctc gaa gac tct 144
Asn Leu Phe Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser
35 40 45

aaa ttg gac aag aag tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt 192
Lys Leu Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu
50 55 60

tat tca gac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta 234
Tyr Ser Asp Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

taaaactacc gtgacgtctt ctactcgact ctgtgctacc tggcttgatc tttgattggc 294

gtgtgcgctt cactggttat gaaccgatct gatcctactc tctgaagacc tctggggtcc 354

aacatccaaa taaagcgaca tcacaaaaaa aaaaaaaaaa aaaaaa 400

<210> 339
<211> 76
<212> PRT
<213> Conus episcopatus

<400> 339
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
20 25 30

Phe Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser Lys Leu
35 40 45

Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
50 55 60

Asp Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
65 70 75

<210> 340
<211> 25
<212> PRT
<213> Conus episcopatus

<220>
<221> SITE
<222> (1)..(25)
<223> Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residues
12 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s

ulpho-Tyr or O-phospho-Tyr

<400> 340
Cys Leu Gly Phe Gly Xaa Ala Cys Leu Met Leu Xaa Ser Asp Cys Cys
1 5 10 15

Ser Xaa Cys Val Ala Leu Val Cys Leu
20 25

<210> 341
<211> 404
<212> DNA
<213> Cerus episcopatus

<220>
<221> CDS
<222> (7)..(240)

<400> 341
ggatcc atg aaa ctg acg tgc gtg gtg atc att gct gtg ctg ttc ttg 48
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu
1 5 10

acc gcc tgg aca ttc gtc atg gct gat gac ccc aga gat gaa ccg gag 96
Thr Ala Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu
15 20 25 30

gca cgt gac gaa atg aac ccc gca gcc tct aaa ttg aac gag aga ggc 144
Ala Arg Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly
35 40 45

tgc ctt gca gtt gat tat ttt tgc ggc ata ccg ttt gtg agc aac ggg 192
Cys Leu Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly
50 55 60

tta tgc tgc agt ggc aat tgt gtt ttt gtc tgc aca ccc caa ggg aag 240
Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
65 70 75

taaaactgcc gtgacgtcct ctactccact ctgtgctacc tggcttgatc tttgattggc 300

gtgtgcactt cactggttat gaatcccctct gatcctactc tctgaagacc tctggggtcc 360

aaacatccaaa taaagcgaca tcccaaaaaa aaaaaaaaaa aaaa 404

<210> 342
<211> 78
<212> PRT
<213> Cerus episcopatus

<400> 342
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg
20 25 30

Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
35 40 45

Ala Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Ser Asn Gly Leu Cys
50 55 60

Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys

65 70 75

<210> 343
<211> 31
<212> PRT
<213> Conus episcopatus

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residue 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12 and 30 may b
e Pro or hydroxy-Pro

<400> 343
Gly Cys Leu Ala Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Ser Asn
1 5 10 15

Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
20 25 30

<210> 344
<211> 202
<212> DNA
<213> Conus achatinus

<220>
<221> CDS
<222> (85)..(171)

<400> 344
aaatcctctg tcctccatct attattattc gctgccaaac tgtgttaaat attcaagtct 60

ctcttttctgt ttgtgtctaa cagg ttg aga tgg tgc att cct aga ggt gat 111
Leu Arg Trp Cys Ile Pro Arg Gly Asp
1 5

ctt tgt ttc ccc tcg gat cgc ata caa tgc tgc agt ggc aag tgc aca 159
Leu Cys Phe Pro Ser Asp Arg Ile Gln Cys Cys Ser Gly Lys Cys Thr
10 15 20 25

ttc gtc tgc atg taaaactgcc gtgatgtctt ctcctccccc c 202
Phe Val Cys Met

<210> 345
<211> 29
<212> PRT
<213> Conus achatinus

<400> 345
Leu Arg Trp Cys Ile Pro Arg Gly Asp Leu Cys Phe Pro Ser Asp Arg
1 5 10 15

Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

<210> 346
<211> 27
<212> PRT
<213> Conus achatinus

<220>
<221> SITE
<222> (1)..(27)

<400> 346
Xaa Cys Ile Xaa Arg Gly Asp Leu Cys Phe Xaa Ser Asp Arg Ile Gln
1 5 10 15

Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

<210> 347
<211> 202
<212> DNA
<213> Conus achatinus

<220>
<221> CDS
<222> (55)..(171)

<400> 347
cgatcctctg tcctcctcct tcattcattc gctgccaaac tgtattaaat attcgaatct 60

ttttttctgt ttgtgtctga caga ttg aga ggg tgc gtt cct agt ggt gaa 111
Leu Arg Gly Cys Val Pro Ser Gly Glu
1 5

att tgt tac ttc atg gat cac ata gga tgc tgc agt ggc aag tgc aca 159
Ile Cys Tyr Phe Met Asp His Ile Gly Cys Cys Ser Gly Lys Cys Thr
10 15 20 25

ttc gtc tgc atg taaaactgcc gtgatgtctt ctcctcccat c 202
Phe Val Cys Met

<210> 348
<211> 29
<212> PRT
<213> Conus achatinus

<400> 348
Leu Arg Gly Cys Val Pro Ser Gly Glu Ile Cys Tyr Phe Met Asp His
1 5 10 15

Ile Gly Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

<210> 349
<211> 27
<212> PRT
<213> Conus achatinus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 349
Gly Cys Val Xaa Ser Gly Xaa Ile Cys Xaa Phe Met Asp His Ile Gly
1 5 10 15

Lys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

<210> 350
<211> 264
<212> DNA
<213> Conus bullatus

<220>
<221> CDS
<222> (1)..(234)

<400> 350
atg aaa ctg acg tgc gtg atg atc gtt act gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aca tat gga ttg aag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Thr Tyr Gly Leu Lys Asn Leu
20 25 30

ttg ccg aac gga cgt cat gaa atg atg aac ccc gaa gcc cct aaa ttg 144
Leu Pro Asn Gly Arg His Glu Met Met Asn Pro Glu Ala Pro Lys Leu
35 40 45

aac aag aaa gat gaa tgc tct gct cct ggt gca ttt tgt ctc atc agg 192
Asn Lys Lys Asp Glu Cys Ser Ala Pro Gly Ala Phe Cys Leu Ile Arg
50 55 60

cca gga ctc tgc tgc agc gag ttc tgc ttc ttt gcg tgt ttt 234
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Phe Ala Cys Phe
65 70 75

taatgacggt tgatgtcttc tactccctc 264

<210> 351
<211> 78
<212> PRT
<213> Conus bullatus

<400> 351
Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Thr Tyr Gly Leu Lys Asn Leu
20 25 30

Leu Pro Asn Gly Arg His Glu Met Met Asn Pro Glu Ala Pro Lys Leu
35 40 45

Asn Lys Lys Asp Glu Cys Ser Ala Pro Gly Ala Phe Cys Leu Ile Arg
50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Phe Ala Cys Phe
65 70 75

<210> 352
<211> 27
<212> PRT
<213> Conus bullatus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residues 2 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residues 6 and 14 may be Pro or hydroxy-Pro

<400> 352
Asp Xaa Cys Ser Ala Xaa Gly Ala Phe Cys Leu Ile Arg Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Phe Ala Cys Phe
20 25

<210> 353
<211> 276
<212> DNA
<213> Conus bullatus

<220>
<221> CDS
<222> (1)..(246)

<400> 353
atg aaa ctg acg tgc gtg atg atc gtt act gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga gac gct ccg gat agt gca 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala
20 25 30

gaa gga tgg gag aaa ctt ttc tcg gag gca cgt gac gaa atg aag aac 144
Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn
35 40 45

agc aaa gac ttt gaa ttg aga ggg tgc ctt cct agg tgg gaa ttt tgt 192
Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys
50 55 60

ccc atc ttt aaa aaa aac gat tgc tgc agt ggc ata tgc ata agc atc 240
Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile
65 70 75 80

tgc ttg taaaactccg tgatgtcttc tcttcccatc 276
Cys Leu

<210> 354
<211> 82
<212> PRT
<213> Conus bullatus

<400> 354
Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala
20 25 30

Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn
35 40 45

Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys
50 55 60

Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile
65 70 75 80

Cys Leu

<210> 355

<400> 355
Gly Cys Leu Xaa Arg Xaa Xaa Phe Cys Xaa Ile Phe Lys Lys Asn Asp
1 5 10 15

Cys Cys Ser Gly Ile Cys Ile Ser Ile Cys Leu
20 25

<210> 356
<211> 268
<212> DNA
<213> Conus striolatus

<220>
<221> CDS
<222> (1)..(237)

<400> 356
atg aaa ctg acg tgc atg atg att gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg ata ttt gta atg gct gat gac tcc aga aat gga ttg gag aat ctt 96
Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

cct cag act aca cgt cac gaa atg aag aac ccc gaa gcc tct aaa ttg 144
Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

aac cag aca gac tgc ctt gct aaa gac gct ttc tgt gcc tgg ccg ata 192
Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile
50 55 60

ctt gga cca ctg tgc tgc agt cgc ttg tgc tta tac gtc tgc atg 237
Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
65 70 75

taaaactgcc gtgatgtctt ctactccccc c 268

<210> 357
<211> 79
<212> PRT
<213> Conus striolatus

<400> 357
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

```
Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile
     50                  55                  60

Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
 65                  70                  75

<210>  358
<211>  19
<212>  PRT
<213>  Conus striolatus

<220>
<221>  SITE
<222>  (1)..(28)
<223>  Xaa at residue 11 may be Trp or bromo-Trp; Xaa at residues 12 and
       16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be Tyr, 125-
       I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.

<400>  358
Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa
 1               5                  10                  15

Leu Cys Cys Ser Arg Leu Cys Leu Xaa Val Cys Met
            20                  25

<210>  359
<211>  266
<212>  DNA
<213>  Conus consors

<220>
<221>  CDS
<222>  (1)..(246)

<400>  359
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc        48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
 1               5                  10                  15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt        96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
            20                  25                  30

tct ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tcg       144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
        35                  40                  45

aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac       192
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
    50                  55                  60

gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca       240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65                  70                  75                  80

ttt tcg tgatgtcttc tcctcccctc                                        266
Phe Ser

<210>  360
<211>  81
<212>  PRT
<213>  Conus consors

<400>  360
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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
            20                  25                  30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
        35                  40                  45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
    50                  55                  60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65                  70                  75                  80

Phe Ser
```


<210> 361
<211> 31
<212> PRT
<213> Conus consors

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 361
Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
1   5   10   15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
            20   25   30

<210> 362
<211> 289
<212> DNA
<213> Conus consors

<220>
<221> CDS
<222> (1)..(252)

<400> 362
atg aaa ctg acg tgc ctg atg atc gtt gct gtg ctg ttc ttg acc acc   48
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Thr
1   5   10   15

tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt   96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
            20   25   30

ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg   144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35   40   45

aat aag aga gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt   192
Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
    50   55   60

tta gga ctc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt   240
Leu Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
```
```

65 70 75 80

gtt gat tct ggc taacagtgtg cgttggttga tgtcttctac tcccctc 289
Val Asp Ser Gly

<400> 363
Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Thr
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
20 25 30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
35 40 45

Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
50 55 60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65 70 75 80

Val Asp Ser Gly

<210> 364
<211> 33
<212> PRT
<213> Conus consors

<220>
<221> SITE
<222> (1)..(32)
<223> Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
Xaa at residue 25 may be Trp or bromo-Trp

<400> 364
Asp Gly Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser
20 25 30

<210> 365
<211> 205
<212> DNA
<213> Conus circumcisus

<220>
<221> CDS
<222> (83)..(175)

<400> 365
gaatccatct gtccatccat ctattcattc attggctgcc aaactgtatt aaatattcaa 60

gtcctctctt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10

```
gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc aag tgc      160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
                15                  20                  25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcttccctc                205
Ala Phe Val Cys Leu
            30

<210>  366
<211>  31
<212>  PRT
<213>  Conus circumcisus

<400>  366
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1               5                  10                  15

Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
            20                  25                  30

<210>  367
<211>  26
<212>  PRT
<213>  Conus circumcisus

<220>
<221>  SITE
<222>  (1)..(26)
<223>  Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

<400>  367
Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
1               5                  10                  15

Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
            20                  25

<210>  368
<211>  206
<212>  DNA
<213>  Conus circumcisus

<220>
<221>  CDS
<222>  (3)..(175)

<400>  368
cgatccatct gtccatccat ctattcattc attcgctgtc aaactgtatt aaatattcaa     60

gtctctcttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt      112
                         Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
                         1               5                  10

gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc agt gcc aag tgc      160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
                15                  20                  25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctactcccct c               206
Ala Phe Val Cys Leu
            30

<210>  369
<211>  31
<212>  PRT
```

<213> Conus circumcisus

<400> 369
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25 30

<210> 370
<211> 27
<212> PRT
<213> Conus circumcisus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
1 may be Pro or hydroxy-Pro

<400> 370
Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
1 5 10 15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25

<210> 371
<211> 206
<212> DNA
<213> Conus circumcisus

<220>
<221> CDS
<222> (33)..(175)

<400> 371
gtatccatct gtccatccat ctattcattc attcgctgtc aaactgtatt aaatattcaa 60

gtctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10

gat cct tgt ttc ccc tcg gat cac ata caa tgc tgc agt gcc aag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcctccact c 206
Ala Phe Val Cys Leu
30

<210> 372
<211> 31
<212> PRT
<213> Conus circumcisus

<400> 372
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25 30

<210> 373

<211> 26
<212> PRT
<213> Conus circumcisus

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

<400> 373
Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
1 5 10 15

Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25

<210> 374
<211> 206
<212> DNA
<213> Conus circumcisus

<220>
<221> CDS
<222> (93)..(175)

<400> 374
cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa 60

tcctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10

gat ctt tgt ttc ccc tcg gat cac ata taa tgc tgc aat gcc gag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Glu Cys
15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcctccctc c 206
Ala Phe Val Cys Leu
30

<210> 375
<211> 31
<212> PRT
<213> Conus circumcisus

<400> 375
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Glu Cys Ala Phe Val Cys Leu
20 25 30

<210> 376
<211> 26
<212> PRT
<213> Conus circumcisus

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro; Xaa at residu
e 20 may be Glu or gamma-carboxy-Glu

<400> 376

Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
1 5 10 15

Cys Asn Ala Xaa Cys Ala Phe Val Cys Leu
20 25

<210> 377
<211> 206
<212> DNA
<213> Conus circumcisus

<220>
<221> CDS
<222> (83)..(175)

<400> 377
ggattcatct gtccatccat ctattcattc attcgctgtc aaactgtatt aaatattcaa 60

gtctatctct ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
1 5 10

gat ctt tgt ttc ccc tcg gat cac ata cga tgc tgc agt gcc aag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Arg Cys Cys Ser Ala Lys Cys
15 20 25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcttcccat c 206
Ala Phe Val Cys Leu
30

<210> 378
<211> 31
<212> PRT
<213> Conus circumcisus

<400> 378
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Arg Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25 30

<210> 379
<211> 27
<212> PRT
<213> Conus circumcisus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
1 may be Pro or hydroxy-Pro

<400> 379
Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Arg
1 5 10 15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
20 25

<210> 380
<211> 206
<212> DNA
<213> Conus circumcisus

<220>
<221> CDS
<222> (83)..(175)

<400> 380
cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa 60

gtctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt 112
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
1 5 10

gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc aag tgc 160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
15 20 25

gca ttc gcc tgc ttg taaaactgcc gtgatgtctt ctcttccgct c 206
Ala Phe Ala Cys Leu
30

<210> 381
<211> 31
<212> PRT
<213> Conus circumcisus

<400> 381
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
20 25 30

<210> 382
<211> 26
<212> PRT
<213> Conus circumcisus

<220>
<221> SITE
<222> (1)..(26)
<223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.

<400> 382
Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
1 5 10 15

Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
20 25

<210> 383
<211> 206
<212> DNA
<213> Conus circumcisus

<220>
<221> CDS
<222> (83)..(175)

<400> 383
cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa 60

gtctctcttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt 112
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
1 5 10

```
gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc aag tgc      160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
                15                  20                  25

gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctactccccc c              206
Ala Phe Val Cys Leu
            30

<210>  384
<211>  31
<212>  PRT
<213>  Conus circumcisus

<400>  384
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
1               5                   10                  15

Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
            20                  25                  30

<210>  385
<211>  27
<212>  PRT
<213>  Conus circumcisus

<220>
<221>  SITE
<222>  (1)..(27)
<223>  Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
       1 may be Pro or hydroxy-Pro

<400>  385
Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
1               5                   10                  15

Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
            20                  25

<210>  386
<211>  260
<212>  DNA
<213>  Conus circumcisus

<220>
<221>  CDS
<222>  (77)..(169)

<400>  386
cgatcctctg ttctcctcta ttattattcg ctgccaactg tattaaatat tcaagtctct      60

ctttctgttt gtgtct aac aga ttg agt tgg tgc att cct act ggt gat ctt      112
                  Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu
                  1               5                   10

tgt ttc ccc tcg gat cac ata caa tgc tgc agt ggc aag tgc aca ttc      160
Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe
        15                  20                  25

gtc tgc atg taaaactgcc gtgatgtctt ctctctcctt c                      200
Val Cys Met
    30

<210>  387
<211>  31
```

<212> PRT
<213> Conus circumcisus

<400> 387
Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu Cys Phe Pro Ser
1 5 10 15

Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25 30

<210> 388
<211> 27
<212> PRT
<213> Conus circumcisus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residue1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
1 may be Pro or hydroxy-Pro

<400> 388
Xaa Cys Ile Xaa Thr Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
1 5 10 15

Lys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
20 25

<210> 389
<211> 266
<212> DNA
<213> Conus monachus

<220>
<221> CDS
<222> (1)..(246)

<400> 389
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

tct ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tcg 144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac 192
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

ggg gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

ttt tcg tgatgtcttc tcctcccctc 266
Phe Ser

<210> 390
<211> 82
<212> PRT

<213> Conus monachus

<400> 390
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Phe Ser

<210> 391
<211> 31
<212> PRT
<213> Conus monachus

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 391
Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

<210> 392
<211> 277
<212> DNA
<213> Conus stercusmuscarum

<220>
<221> CDS
<222> (1)..(246)

<400> 392
atg aaa ctg acg tgc atg atg atc gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc aca gct gat gac tcc ata aat gga ccg gag aat aga 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
20 25 30

cga ata tgg gag aaa ctt ttg ttg aag gca cgt gac gaa atg aag aac 144
Arg Ile Trp Glu Lys Leu Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
35 40 45

ccc gaa gcc tct caa ttg aga tgg tgc att cct agt ggt gaa ctt tgt 192
Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
50 55 60

```
ttc cgc tcg gat cac ata caa tgc tgc agt gcc aag tgc gca ttc gtc      240
Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val
65                  70                  75                  80

tgc ttg taaaactacc gtgatgtctt ctgctcccat c                          277
Cys Leu

<210>  393
<211>  80
<212>  PRT
<213>  Conus stercusmuscarum

<400>  393
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
            20                  25                  30

Arg Ile Trp Glu Lys Leu Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
        35                  40                  45

Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
    50                  55                  60

Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val
65                  70                  75                  80

Cys Leu

<210>  394
<211>  27
<212>  PRT
<213>  Conus stercusmuscarum

<220>
<221>  SITE
<222>  (1)..(27)
<223>  Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be
       Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy
       -Glu

<400>  394
Xaa Cys Ile Xaa Ser Gly Xaa Leu Cys Pro Arg Ser Asp His Ile Gln
1               5                  10                  15

Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
            20                  25

<210>  395
<211>  246
<212>  DNA
<213>  Conus stercusmuscarum

<220>
<221>  CDS
<222>  (1)..(246)

<400>  395
atg aaa ctg acg tgt gtg atg atc gtt gct gtg ctg ttc ttg atc gcc      48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
1               5                  10                  15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg aag aat ctt      96
```

```
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
            20                  25                  30

ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg      144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35                  40                  45

aac aag aga gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cgt      192
Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
    50                  55                  60

cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt      240
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65                  70                  75                  80

att gat tgatgtcttc tattccccta                                       266
Ile Asp

<210> 396
<211> 82
<212> PRT
<213> Conus stercusmuscarum

<400> 396
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
1               5                  10                  15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
            20                  25                  30

Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35                  40                  45

Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
    50                  55                  60

Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
65                  70                  75                  80

Ile Asp

<210> 397
<211> 31
<212> PRT
<213> Conus stercusmuscarum

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 ma
      y be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or br
      omo-Trp

<400> 397
Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu
1               5                  10                  15

Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
            20                  25                  30

<210> 398
<211> 265
<212> DNA
<213> Conus striolatus
```

<220>
<221> CDS
<222> (1)..(234)

<400> 398
atg aaa ctg acg tgc ata atg acc gtt gct gtg ctg ttc ttg acc gct 48
Met Lys Leu Thr Cys Ile Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

ctt ctg aag aca cgt cac gaa gtg gaa aac ccc aaa gcc tct agg tcg 144
Leu Leu Lys Thr Arg His Glu Val Glu Asn Pro Lys Ala Ser Arg Ser
35 40 45

agc ggt agg tgc cgt cct ggt ggt acg gtt tgt ggc ttt ccg aaa cct 192
Ser Gly Arg Cys Arg Pro Gly Gly Thr Val Cys Gly Phe Pro Lys Pro
50 55 60

gga cca tac tgc tgc agt ggc tgg tgc ttt ttt gtc tgc gcc 234
Gly Pro Tyr Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Ala
65 70 75

taaactgcct gtgatgtctt ctcctcccat c 265

<210> 399
<211> 78
<212> PRT
<213> Conus striolatus

<400> 399
Met Lys Leu Thr Cys Ile Met Thr Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Leu Leu Lys Thr Arg His Glu Val Glu Asn Pro Lys Ala Ser Arg Ser
35 40 45

Gly Gly Arg Cys Arg Pro Gly Gly Thr Val Cys Gly Phe Pro Lys Pro
50 55 60

Gly Pro Tyr Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Ala
65 70 75

<210> 400
<211> 27
<212> PRT
<213> Conus striolatus

<220>
<221> SITE
<222> (1)..(27)
<223> Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa a
t residue 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or bro
mo-Trp

<400> 400
Cys Arg Xaa Gly Gly Thr Val Cys Gly Phe Xaa Lys Xaa Gly Xaa Xaa
1 5 10 15

```
Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Ala
            20                  25

<210>  401
<211>  27.
<212>  DNA
<213>  Conus striolatus

<220>
<221>  CDS
<222>  (1)..(243)

<400>  401
atg aaa ctg acg tgc gtg atg atc gtt gct gtg ctg ttc ttg act gcc        48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat        96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
            20                  25                  30

ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg       144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
        35                  40                  45

gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag       192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
    50                  55                  60

ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc ggt       240
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65                  70                  75                  80

ggt taactgccgt gatgtcttct attccccctc                                  272
Gly

<210>  402
<211>  81
<212>  PRT
<213>  Conus striolatus

<400>  402
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
1               5                  10                  15

Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
            20                  25                  30

Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
        35                  40                  45

Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
    50                  55                  60

Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
65                  70                  75                  80

Gly

<210>  403
<211>  29
<212>  PRT
<213>  Conus striolatus
```

<220>
<221> SITE
<222> (1)..(20)
<223> Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be Pro or hydroxy-Pro

<400> 403
Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
1 5 10 15

Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
20 25

<210> 404
<211> 365
<212> DNA
<213> Conus striolatus

<220>
<221> CDS
<222> (1)..(346)

<400> 404
atg aaa ctg acg tgt ctg atg gct gtt gct gtg ctg ttc ttg acc gcc 48
Met Lys Leu Thr Cys Leu Met Ala Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

cgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt 96
Arg Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

tct ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tcg 144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac 192
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
50 55 60

tga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca 240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

ttt tcg tgatgtcttc tatccccctc 265
Phe Ser

<210> 405
<211> 3?
<212> PRT
<213> Conus striolatus

<400> 405
Met Lys Leu Thr Cys Leu Met Ala Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Arg Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
20 25 30

Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
35 40 45

Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn

50 55 60

Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
65 70 75 80

Phe Ser

<100> 406
<211> 31
<212> PRT
<213> Conus striolatus

<220>
<221> SITE
<222> (1)..(31)
<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be Glu or gamma-carboxy-Glu

<400> 406
Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
1 5 10 15

Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
20 25 30

<210> 407
<211> 237
<212> DNA
<213> Conus striolatus

<220>
<221> CDS
<222> (1)..(231)

<400> 407
atg aaa ctg acg tgt atg gtg atc gtc gcc gtg ctg ctc ctg acg acc 48
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Thr
1 5 10 15

tgt cat ctc atc aca gct gat gac tcc aga ggt acg cag aag cat cgt 96
Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

tcc ctg agg tcg act acc aaa gtc tcc aag tcg act agc tgc atg aaa 144
Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
35 40 45

gcc ggg tct tat tgc gtc gct act acg aga atc tgc tgc ggt tat tgc 192
Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
50 55 60

gct tat ttc ggc aaa ata tgt att ggc tat ccc aaa aac tgatcctccc 241
Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn
65 70 75

<400> 408 ctactgtgc tctatcattt tctgcctgat gtcttctcct ccctc 287

<210> 408
<211> 77
<212> PRT
<213> Conus striolatus

<400> 408

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Thr
1 5 10 15

Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
35 40 45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
50 55 60

Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn
65 70 75

(210) 409
(211) 35
(212) PRT
(213) Conus striolatus

(220)
(221) SITE
(222) (1)..(35)
(223) Xaa at residues 10, 21, 24 and 32 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 33 may be Pro or hydroxy-Pro

(400) 409
Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg
1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Gly Xaa
20 25 30

Xaa Lys Asn
35